

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 7, 2006, 05:45:42 ; Search time 385.92 Seconds
(without alignments)
12822.754 Million cell updates/sec

Title: US-10-767-521-2

Perfect score: 1065

Sequence: 1 atgacaacctcactagatcac.....cgaacctctcattgtgttc 1065

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST: *
1: gb_est1: *
2: gb_est2: *
3: gb_est3: *
4: gb_htc: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_est7: *
9: gb_gss1: *
10: gb_gss2: *
11: gb_gss3: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1065	100.0	1098	11 DQ030562	DQ030562 Homo sapi
2	835	78.4	867	7 CN837388	CN837388 AGENCOURT
3	816.4	76.7	1002	7 CN801748	CN801748 ILLUMIGEN
c 4	784	73.6	793	7 CN837645	CN837645 AGENCOURT
5	748.8	70.3	789	2 BG205056	BG205056 RST24475
6	713	66.9	884	2 BG182330	BG182330 RST1196 A
7	703.8	66.1	876	3 BI906283	BI906283 603063222
8	681.4	64.0	702	7 CO960092	CO960092 AGENCOURT
9	669.8	62.9	675	7 CV030237	CV030237 9286 Full
10	660	62.0	1761	4 AK041106	AK041106 Mus muscu
11	653.6	61.4	2284	4 AK089875	AK089875 Mus muscu
12	653.6	61.4	2396	4 AK089895	AK089895 Mus muscu
13	651.6	61.2	745	4 BG204024	BG204024 RST23417
14	540.8	50.8	1086	10 AY399291	AY399291 Homo sapi
15	540.8	50.8	2583	4 CR609171	CR609171 full-length
16	523.4	49.1	1030	11 DQ030563	DQ030563 Pan trogl
17	492.8	46.3	690	7 CK949072	CK949072 4074244 B
18	479.8	45.1	2118	4 AK031109	AK031109 Mus muscu
19	479.2	45.0	1086	10 AY399293	AY399293 Mus muscu
20	479.2	45.0	2292	4 AK036597	AK036597 Mus muscu
21	479.2	45.0	2432	4 AK036690	AK036690 Mus muscu
22	474.6	44.6	962	1 AL552677	AL552677 AL552677

c	23	474.4	44.5	2708	4 AK076275	AK076275 Mus muscu
	24	455.6	42.8	750	7 CO960088	CO960088 AGENCOURT
	25	455.2	42.7	832	7 CN155784	CN155784 943112 MA
	26	446.4	41.9	653	7 CN793072	CN793072 4128034 B
	27	439.2	41.2	983	5 BX337412	BX337412 BX337412
	28	437.2	41.1	934	2 BG460984	BG460984 RST43688
	29	432	40.6	1074	3 BM917063	BM917063 AGENCOURT
	30	418.8	39.3	731	7 CK954144	CK954144 4094053 B
	31	410.8	38.6	881	2 BG460103	BG460103 RST42555
c	32	396	37.2	815	7 CO958981	CO958981 AGENCOURT
	33	383.8	36.0	816	5 BX340358	BX340358 BX340358
	34	376.6	35.4	1065	10 AY399290	AY399290 Mus muscu
	35	363.6	34.1	687	6 CF768885	CF768885 CES001048
	36	363.4	34.1	1059	10 AY399288	AY399288 Homo sapi
	37	362.6	34.0	1059	10 AY399289	AY399289 Pan trogl
	38	350.4	32.9	1083	10 AY398810	AY398810 Mus muscu
	39	350.4	32.9	2267	4 AK046579	AK046579 Mus muscu
	40	349.2	32.8	727	5 BY751590	BY751590 BY751590
	41	348.8	32.8	1083	10 AY398808	AY398808 Homo sapi
	42	344	32.3	1083	10 AY398809	AY398809 Pan trogl
c	43	330.8	31.1	657	7 CO683220	CO683220 DG11-166f
	44	325	30.5	581	3 BP306915	BP306915 BP306915
	45	324	30.4	733	8 DN996892	DN996892 TC119287

ALIGNMENTS

RESULT 1
DQ030562
LOCUS
DEFINITION Homo sapiens CCR3 gene, VIRUTAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION DQ030562
VERSION DQ030562.1 GI:66881766
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1098)
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE A Scan for Positively Selected Genes in the Genomes of Humans and Chimpanzees
JOURNAL PLoS Biol. 3 (6), E170 (2005)
PUBMED 15869325
REFERENCE 2 (bases 1 to 1098)
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of alignment.
FEATURES
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 7e-297;
Matches 1065; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      151 TACTCCCTGCTGTCTCACTGTGGGCTCTTTGGGCAATGTGTGTGTGATGATCTCTCAT 210
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QY      241 CTGCTCTTCTCGTCAACCCCTTCATTCTGGATCCATATGTACAGGGGCAATACTGGGTT 300
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Db      751 ATTTTGTATCATGCGGTGTTTTCATTTTCTGACACCCCTACAAATGTGCTATCCTT 810
QY      781 CTCTCTTCTATCAATCCATCTTATTTGAAATGACTGTGACGAGCAACATCTGAC 840
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QY      841 CTGTCATGCTGTGACAGAGGTATCGCCTAATCCCACTGCTGCATGAACCCGGTGATC 900
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Db      871 CTGTCATGCTGTGACAGAGGTATCGCCTAATCCCACTGCTGCATGAACCCGGTGATC 930
QY      901 TAGGCTTTGTGAGAGAGGTTCGGAAGTACCTGCGCACTTTTCCACAGGCACTTG 960
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QY      961 CTGATGACCTGGGAGATATCATCCCAATCTTCTCTAGTGAGAGGCTGAAAAAGACAGC 1020
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Db      991 CTGATGACCTGGGAGATATCATCCCAATCTTCTCTAGTGAGAGGCTGAAAAAGACAGC 1050
QY      1021 TCTGTCTCTCCATCCACAGCAGAGCCGGAATCTCTATTTGTGTTT 1065
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Db      1051 TCTGTCTCTCCATCCACAGCAGAGCCGGAATCTCTATTTGTGTTT 1095
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RESULT 2
CN837388
LOCUS
DEFINITION
AGENCOURT_15864186 NIH_MGC_145 Homo sapiens cDNA clone
IMAGE:7001957 3', mRNA sequence.
CN837388
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 867)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: GPCR Consortium
cDNA Library Preparation: GPCR Consortium
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: IRB13 row: c column: 03
High quality sequence stop: 708.
Location/Qualifiers
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FEATURES

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/clone="IMAGE:7001957"
/tissue_type="mixed"
/lab_host="DH10B"
/clone_lib="NIH_MGC_145"
/note="Vector: pCDNA3.1 Site 1: varies by clone; Site 2:
varies by clone; ORFs were PCR-amplified and cloned into
pCDNA3.1 by the GPCR Consortium. Cloning sites vary by
clone and include the following: 5'-BcorV-Xmnl/Xho1-3',
5'-BcorV-Xmnl/NotI-3', BcorV (TA cloned, non-directional).
For information about which gene each clones represents,
please visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearayed_plates/IRB1.presv.dat
a Note: this is a NIH_MGC Library."
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ORIGIN

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Query Match 78.4%; Score 835; DB 7; Length 867;
Best Local Similarity 99.1%; Pred. No. 3.1e-230;
Matches 849; Conservative 0; Mismatches 7; Indels 1; Gaps 1;
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Db      11 ATGACAACCTCACTAGATACAGTTGAGACCTTTGGTACCACATCCTACTATGATGACGTG 70
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Db      71 GGCCCTGCTCTGTGAAAAAGCTGATATACAGACCACTGATGCCCCAGTTGTGTGCCCGCTG 130
QY      121 TACTCCCTGCTGTCTCACTGTGGGCTCTTTGGGCAATGTGTGTGTGATGATCTCTCAT 180
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Db      131 TACTCCCTGCTGTCTCACTGTGGGCTCTTTGGGCAATGTGTGTGTGATGATCTCTCAT 190
QY      181 AAATACAGAGAGGCTCCGAATTATGACCAACATCTACCTGCTCAACCTGGCCATTTCGGAC 240
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Db      191 AAATACAGAGAGGCTCCGAATTATGACCAACATCTACCTGCTCAACCTGGCCATTTCGGAC 250
QY      241 CTGCTCTTCTCGTCAACCCCTTCATTCTGGATCCATATGTACAGGGGCAATACTGGGTT 300
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Db 251 CTGCTCTTCCTCGTCAACCTTCATCTTGATCCACTATGTACAGGGGCATAACTGGGT 310
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Db 311 TTGGCCATGGCATGTGTAGCTCTCTCAGGGTTTATCAACAAGCTTGTACAGCGAG 370
Qy 361 ATCTTTTTCATATCTCTGTCGACATGACAGAGTACCTGGCCATTGTCCATGCTGTGTT 420
Db 371 ATCTTTTTCATATCTCTGTCGACATGACAGAGTACCTGGCCATTGTCCATGCTGTGTT 430
Qy 421 GCCCTTCGAGCCCGGACTGTCACTTTGGTGTCACTCACAGCATGCTCACCTGGGGCCTG 480
Db 431 GCCCTTCGAGCCCGGACTGTCACTTTGGTGTCACTCACAGCATGCTCACCTGGGGCCTG 490
Qy 481 GCAGTGCTAGCAGCTCTTCTCTGAATTTATCTTATGAGACTGAAGAGTTGTTGAAGAG 540
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Db 551 ACTCTTTGCAGTGCTCTTACCCAGAGATACAGTATATAGCTGAGGCATTTCCACACT 610
Qy 601 CTGAGAATGACCATCTTCTGTCTGTCTCTCCCTGCTGCTGTTATGGCCATCTGTACACA 660
Db 611 CTGAGAATGACCATCTTCTGTCTGTCTCTCCCTGCTGCTGTTATGGCCATCTGTACACA 670
Qy 661 GGAATCATCAAAACGCTGCTGAGGTGCCCCAGTAAAAAAGTACAAGGCCATCCGGCTC 720
Db 671 GGAATCATCAAAACGCTGCTGAGGTGCCCCAGTAAAAAAGTACAAGGCCATCCGGCTC 730
Qy 721 ATTTTGTTCATCATGCGGGT-GTTTTTCATTTTCTGAGACCCCTACAATGTGCTATCCT 779
Db 731 ATTTTGTTCATCATGCGGGT-TTTTCATTTTCTGAGACCCCTACAATGTGCTATCCT 790
Qy 780 TCTCTCTCTCTATCATCATCTTATTTTGAATGACTGTGACCGGAGCAAGCATCTGGA 839
Db 791 TCTCTCTCTCTATNCATCCATCTTATTTGGAATGACTGTGACCGGAGCAAGCATCTGGA 850
Qy 840 CCTGCTCATGCTGTGA 856
Db 851 CCTGCTCATGCTGTGNTA 867

RESULT 3
CN801748 1002 bp mRNA linear EST 26-MAY-2004
LOCUS CN801748
DEFINITION ILUMIGEN MCQ_35976 Katze_MMP1l Macaca mulatta cDNA clone
IBIUM:14674 5' similar to Bases 3 to 1000 highly similar to human
CCR3 (Hs.506190), mRNA sequence.
ACCESSION CN801748
VERSION CN801748.1 GI:47697724
KEYWORDS EST.
SOURCE Macaca mulatta (rhesus monkey)
ORGANISM Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Cercopithecoidea; Cercopithecinae; Macaca.
REFERENCE 1 (bases 1 to 1002)
AUTHORS Magness,C.L., Fellin,P.C., Thomas,M.J., Korth,M.J., Agy,M.B.,
Proll,S.C., Fitzgibbon,M., Scherer,C.A., Miner,D.G., Katze,M.G. and
Iadonato,S.P.
TITLE Analysis of the Macaca mulatta transcriptome and the sequence
divergence between Macaca and human
JOURNAL Genome Biol. 6 (7), R60 (2005)
PUBMED 15998449
COMMENT Contact: C. Magness
illumigen Biosciences Inc.
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
Tel: 2063780400
Fax: 2063780408
Email: cmagness@illumigen.com
Sequenced on 2004.05.11. 688 Q20 bases.

PCR Primers
FORWARD: CCTCACTAAAGGAACAATA
BACKWARD: CACTATAGGGCGAATTGGTA
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Seq primer: CCTCACTAAAGGAACAATA
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/lab_host="E. coli SOLR"
/clone_1lb="Katze_MMP1l"
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Synthesis kit (catalog #200400) and ZAP-CDNA Gigapack III
Gold Cloning kit (Catalog #200450)."

ORIGIN
Query Match 76.7%; Score 816.4; DB 7; Length 1002;
Best Local Similarity 90.1%; Pred. No. 8e-225;
Matches 896; Conservative 0; Mismatches 96; Indels 2; Gaps 2;
Qy 73 GAAAAAGCTGATACCAAGACATGATGGCCAGTTTGTGCCCCGCTGTACTCCCTGGT 132
Db 1 GAAAAAGCCGATGTCGAGACATGATAGCCAGTTCGTGCCCCGCTGTATTCCTGGT 60
Qy 133 TTCATGTGGGCTCTTGGGCAATGTGTGTGTGTATCTCTATAAATACAGAGAG 192
Db 61 TTCATGTGGGCTCTTGGGCAATGTGTGTGTGTATCTCTATAAATACAGAGAG 120
Qy 193 CTCGAATTTATGACCAACATCTACTGCTCAACCTGGCCATTTGGACCTGCTTCTC 252
Db 121 CTCGAATTTATGACCAACATCTACTGCTCAACCTGGCCATTTGGACCTGCTTCTC 180
Qy 253 GTCACTCTTCATTTCTGATTCATATGTGAGGGGCATTAAGGTTTGGCCATGGC 312
Db 181 TTCACCTTCCGTTCTGATTCATATGTGAGGGGCATTAAGGTTTGGCCATGGC 240
Qy 313 ATGTGTAAGCTCTCTCAGGGTTTATACACAGGCTGTACAGGAGATCTTTTCATA 372
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Qy 433 CGGACTGTCACTTTTGGTGTATCAACGATGCTACCTGGGGCTGGCAGTGTAGCA 492
Db 361 AGGACTGTCACTTTTGGTGTATCAACGATGCTACCTGGGGCTGGCAGTGTAGCA 420
Qy 493 GCTCTTCTGAATTTATCTTATGAGACTGAAGAGTTGTTGAAGAGACTCTTTCAGT 552
Db 421 GCTCTTCTGAATTTATCTTATGAGACTGAAGAGTTGTTTCAGAGACTCTTTCAGT 480
Qy 553 GCTCTTACCCAGAGATACAGTATATAGCTGAGGCACTTCCACACTGTGAGATGACC 612
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Qy 613 ATCTTGTGTCTGTTCTCCCTGCTGCTGTATGAGCCATCTGTACACAGGAATCATCAA 672
Db 541 ATCTTGTGTCTGTTCTCCCTGCTGCTGTATGAGCCATCTGTACACAGGAATCATCAA 600
Qy 673 ACGCTGTGAGGTGCCCCAGTAAAAAAGTACAAGGCCATCCGGCTCATTTTGTGATC 732
Db 601 ACGCTGTGAGGTGCCCCAGTAAAAAAGTACAAGGCCATCCGGCTCATTTTGTGATC 660
Qy 733 ATGGCGGTGTTTTCATTTTCTGAGACACCTCAATGTGGCTATCTTCTCTCTCTAT 792

Db 661 ATGGCTGTGTTTTCATTTCTGAGACACCCCTACATGTGGCTATCCTTATCTCTACTAT 720
QY 793 CAATCCATCTTATTTGAAATGACTGTGAGCGGAGCAAGCATCTGACCTGTGTCATGCTG 852
Db 721 CAATCCGCTTATTTGACTTGACTGTGTAACGAGCAAGCATCTGACCTGTTCGTCTG 780
QY 853 GTGACAGAGGTGATCCGCTTACTTCCCACTGCTGTCATGAACCCGGTGATCTACGCCCTTGT 912
Db 781 GCGACGGAAGGATTCCTCTACTCCCACTGCTGCGTGAACCC-GTGATCTACCCCTTGT 839
QY 913 GGAGAGAGGTTCCGGAAGTACTGCGCCCACTTCTCCACAGGCACTTGCTCATGCACTG 972
Db 840 GAAAAAAGGTTCCGGAAGTACTGCGCCCTTCTTCCACAGGCCCGTGTCTTGCCCTG 899
QY 973 GCGAGATACATCCCATTCCTTCTAGTGAGAGCT-GGAAAGAACAGCTCTGTCTCTCC 1031
Db 900 GCGAATATCTTCCCTTCCCTTCTAGGAAAAAAGTGGAGGAACATTTCTGTCCCTCC 959
QY 1032 ATCCACAGCAGAGCCGGAAGCTCTATGTGTTT 1065
Db 960 CTCCCAACAACCCCGAATCTTTTGTGTTT 993

RESULT 4
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LOCUS AGENCOURT_15669744 NIH_MGC_145 Homo sapiens cDNA clone
DEFINITION IMAGE:7001957 5', mRNA sequence.

ACCESSION CN837645
VERSION CN837645
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 793)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITL National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)

COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: GPCR Consortium
cDNA Library Preparation: GPCR Consortium
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: IRB13 row: c column: 03
High quality sequence stop: 649.

FEATURES
source location/Qualifiers
1..793

/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:7001957"
/tissue_type="mixed"
/lab_host="DH10B"
/clone_lib="NIH MGC 145"
/note="Vector: pCDNA3.1; Site 1: varies by clone; Site 2:
varies by clone; ORFs were PCR-amplified and cloned into
pCDNA3.1 by the GPCR Consortium. Cloning sites vary by
clone and include the following: 5'-EcoRV-XmnI/XhoI-3',
5'-EcoRV-XmnI/NotI-3', EcoRV (TA cloned, non-directional).
For information about which gene each clone represents,
please visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearrayed_plates/IRB1.presv.dat
a Note: this is a NIH_MGC Library."

ORIGIN

Query Match 73.6%; Score 784; DB 7; Length 793;
Best Local Similarity 99.4%; Pred. No. 1,8e-215;
Matches 787; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 274 CACTATGTGAGGGGCACTAAGTGGGTTTGGCCATGCAATGTGTAAAGCTCCTCAGGG 333
Db 793 CACTATGTGAGGGGCACTAAGTGGGTTTGGCCATGCAATGTGTAAAGCTCCTCAGGG 734
QY 334 TTTTATCACACAGGCTTGTAACGAGATCTTTTCAATATCCTGCTGACAAATGACAGG 393
Db 733 TTTTATCACACAGGCTTGTAACGAGATCTTTTCAATATCCTGCTGACAAATGACAGG 674
QY 394 TACCTGGCCATTTGTCATGCTGTGTTTGCCCTTGAGCCCGGACTGTCACTTTGTGTC 453
Db 673 TACCTGGCCATTTGTCATGCTGTGTTTGCCCTTGAGCCCGGACTGTCACTTTGTGTC 614
QY 454 ATCAACAGCATGCTCACTGGGGCTGGCAGTGTGACAGCTCTTCTGAATTTATCTTC 513
Db 613 ATCAACAGCATGCTCACTGGGGCTGGCAGTGTGACAGCTCTTCTGAATTTATCTTC 554
QY 514 TATGAGACTGAAGAGTTGTTGAAGAGACTCTTTGCAATGCTCTTTACCCAGAGATACA 573
Db 553 TATGAGACTGAAGAGTTGTTGAAGAGACTCTTTGCAATGCTCTTTACCCAGAGATACA 494
QY 574 GTATATAGCTGAGGCACTTTCACACTCTGAGAAATGACATCTTGTCTCGTTCTCCCT 633
Db 493 GTATATAGCTGAGGCACTTTCACACTCTGAGAAATGACATCTTGTCTCGTTCTCCCT 434
QY 634 CTGCTCGTTATGCGCATCTGCTACACAGGAATCATCAAAACGCTGAGGTGCCCACT 693
Db 433 CTGCTCGTTATGCGCATCTGCTACACAGGAATCATCAAAACGCTGAGGTGCCCACT 374
QY 694 AAAAAAAGTACAAAGGCCATCCGCTCATTTTGTGATCATGCGGTGTTTTCATTTTC 753
Db 373 AAAAAAAGTACAAAGGCCATCCGCTCATTTTGTGATCATGCGGTGTTTTCATTTTC 314
QY 754 TGGACACCCCTACATGTGGCTATCTTCTCTCTTCAATCCATCTTATTTGAAAT 813
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QY 814 GACTGTAGCGGAGCAAGCATCTGGAACCTGTCATGCTGTGACAGAGGTATCGCCTAC 873
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QY 934 CTGGCCCACTTCTTCCACAGGCACTTGTCTATGACACCTGGGCAAGATACCCATCTCT 993
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QY 994 CCTAGTGAAGAGCTGGAAGAACAAGCTCTGTCTCTCCATCCACAGAGCCGGAAGTAC 1053
Db 73 CCTAGTGAAGAGCTGGAAGAACAAGCTCTGTCTCTCCATCCACAGAGCCGGAAGTAC 14
QY 1054 TCTATGTGTTT 1065
Db 13 TCTATGTGTTT 2

RESULT 5
LOCUS BG205056 789 bp mRNA linear EST 21-APR-2001
DEFINITION RST24475 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION BG205056
VERSION BG205056.1 GI:13726743
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 789)
AUTHORS Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whitcington,J., Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher,J., Danzig,J. and Ducar,M.
TITLE Creation of genome-wide protein expression libraries using random activation of gene expression
JOURNAL Nat. Biotechnol. 19 (5), 440-445 (2001)
PUBMED 11329013
COMMENT Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@athersys.com
High quality sequence stop: 521.
FEATURES
source
1. .789
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_line="HT1080"
/clone_lib="Athersys RAGE Library"
/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."
ORIGIN
Query Match 70.3%; Score 748.8; DB 2; Length 789;
Best Local Similarity 98.6%; Pred. No. 2.9e-205;
Matches 764; Conservative 0; Mismatches 10; Indels 1; Gaps 1;
QY 1 ATGACAACCTCACTAGATACAGTTGAGACCTTTGGTACCACTCTATGATGACGTG 60
Db 16 ATGACAACCTCACTAGATACAGTGAAGACCTTTGGTACCACTCTATGATGACGTG 75
QY 61 GGCGTCTCTGTGAAAAAGCTGATACCAGAGCACTGATGGCCCAAGTTGTGCCCGCTG 120
Db 76 GGCGTCTCTGTGAAAAAGCTGATACCAGAGCACTGATGGCCCAAGTTGTGCCCGCTG 135
QY 121 TACTCCCTGTGTCTCACTGTGGGCTCTTTGGCAATGTGTGTGTGATGATCTCTATA 180
Db 136 TACTCCCTGTGTCTCACTGTGGGCTCTTTGGCAATGTGTGTGTGATGATCTCTATA 195
QY 181 AAATACAGAGGCTCCGAATTATGACCAACATCTACCTGCTCAACCTGGCCATTTCGAC 240
Db 196 AAATACAGAGGCTCCGAATTATGACCAACATCTACCTGCTCAACCTGGCCATTTCGAC 255
QY 241 CTGCTCTTCTCGTCAACCTTCATCTTGATCCACTATGTCAAGGGGCATTAACCTGGCTT 300
Db 256 CTGCTCTTCTCGTCAACCTTCATCTTGATCCACTATGTCAAGGGGCATTAACCTGGCTT 315
QY 301 TTGGCCATGGCATGTGAAGCTCCTCTCAGGGTTTATCACACAGGCTTGTACAGCAG 360
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QY 361 ATCTTTTTCATATCCTGCTGACATCGACAGGATCCTGGCCATTGTCCATGCTGTGTT 420
Db 376 ATCTTTTTCATATCCTGCTGACATCGACAGGATCCTGGCCATTGTCCATGCTGTGTT 435
QY 421 GCCCTTCGAGCCCGGACTGTCACTTTGGTGTATCATCACAGCATCGTCACTGGGGCTG 480
Db 436 GCCCTTCGAGCCCGGACTGTCACTTTGGTGTATCATCACAGCATCGTCACTGGGGCTG 495
QY 481 GCAGTGTAGCAGCTCTTCTGGAATTATCTTCTATGAGACTGAAGAGTTGTTGAAGAG 540
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QY 541 ACTCTTTCAGTGTCTCTTTACCCAGAGATACAGTATATAGCTGGAGCATTTCCACACT 600
Db 556 ACTCTTTCAGTGTCTCTTTACCCAGAGATACAGTATATAGCTGGAGCATTTCCACACT 615
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QY 661 GGAATCATCAAAACGCTGCTGAGGTGCCCCAGTAAAAAAGTACAAGGCCATCCGGCTC 720
Db 676 GGAATCATCAAAACGCTGCTGAGGTGCCCCAGTAAAAAAGTACAAGGCCATCCGGCTC 735
QY 721 ATTTTGTATCATGCGCGGTGTTTTCATTCTTGACACACCTACATGTGCTA 775
Db 736 ATTTTGTATCATGCGCGGTGTTTTCATTCTT-GACACCTACATGTGCTA 789
RESULT 6
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LOCUS
DEFINITION RST1196 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION BG182330
VERSION BG182330.1 GI:13704017
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 884)
AUTHORS Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whitcington,J., Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher,J., Danzig,J. and Ducar,M.
TITLE Creation of genome-wide protein expression libraries using random activation of gene expression
JOURNAL Nat. Biotechnol. 19 (5), 440-445 (2001)
PUBMED 11329013
COMMENT Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@athersys.com
High quality sequence stop: 529.
FEATURES
source
1. .884
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_line="HT1080"
/clone_lib="Athersys RAGE Library"
/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."
ORIGIN
Query Match 66.9%; Score 713; DB 2; Length 884;
Best Local Similarity 98.3%; Pred. No. 7.2e-195;
Matches 742; Conservative 0; Mismatches 10; Indels 3; Gaps 2;
QY 1 ATGACAACCTCACTAGATACAGTTGAGACCTTTGGTACCACTCTATGATGACGTG 60
Db 17 ATGACAACCTCACTAGATACAGTTGAGACCTTTGGTACCACTCTATGATGACGTG 76
QY 61 GGCGTCTCTGTGAAAAAGCTGATACCAGAGCACTGATGGCCCAAGTTGTGCCCGCTG 120
Db 77 GGCGTCTCTGTGAAAAAGCTGATACCAGAGCACTGATGGCCCAAGTTGTGCCCGCTG 136

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QY 121 TACCCCTGCTGTTCACTGTGGGCTCTTGGGCAATGTGTGTGATGATCTCTATA 180
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Db 137 TACTCCCTGTGTTCACTGTGGGCTCTTGGGCAATGTGTGTGATGATCTCTATA 196
QY 181 AAATACAGAGGCTCCGAATTATGACCAACATCTACCTGTCAACCTGGCCATTTCGAC 240
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Db 197 AAATACAGAGGCTCCGAATTATGACCAACATCTACCTGTCAACCTGGCCATTTCGAC 256
QY 241 CTGCTCTTCTCTGTCACCCCTTCCATTCTGGATCCACTATGTCAAGGGGCATACTGGGTT 300
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Db 257 CTGCTCTTCTCTGTCACCCCTTCCATTCTGGATCCACTATGTCAAGGGGCATACTGGGTT 316
QY 301 TTGGCCATGCGCATGTGTAACTCTCTCAGGGTTTATCAGACAGGCTGTACAGCGAG 360
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Db 317 TTGGCCATGCGCATGTGTAACTCTCTCAGGGTTTATCAGACAGGCTGTACAGCGAG 376
QY 361 ATCTTTTTCATTAATCTGTGCAATCGACAGGTACCTGGCCATTGTCCATGTGTGTT 420
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Db 377 ATCTTTTTCATTAATCTGTGCAATCGACAGGTACCTGGCCATTGTCCATGTGTGTT 436
QY 421 GCCCTTCGAGCCCGGACTGTCACTTTGGTGTATCACCAGCATCTGACCTGGGCGCTG 480
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Db 437 GCCCTTCGAGCCCGGACTGTCACTTTGGTGTATCACCAGCATCTGACCTGGGCGCTG 496
QY 481 GCAATGCTAGCAGCTCTTCCGTAATTATCTTATGAGACTGAAGTTGTTGAAGAG 540
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Db 497 GCAATGCTAGCAGCTCTTCCGTAATTATCTTATGAGACTGAAGTTGTTGAAGAG 556
QY 541 ACTCTTTGCAAGTGTCTTTTACCCAGAGGATACAGTATATAGCTGAGGCAATTCCACT 600
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Db 557 ACTCTTTGCAAGTGTCTCTTACCAGAGGATACAGTATATAGCTGAGGCAATTCCACT 616
QY 601 CTGAGAATGACCATCTTCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 660
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Db 617 CTGAGAATGACCATCTTCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 676
QY 661 GGAATCATCAAAACGCTGTGAGGTGCCCCAGTAAAAAAAGTACAAGGCCATCCGGCTC 720
    |||||||
Db 677 GGAATCATC-AAACGCTGTGAGGTGCCCCAGTAAAAAG--ACAGGCCATCCGGCTC 733
QY 721 ATTTTGTTCATCATGCGGTGTTTTCATTTTCTG 755
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Db 734 ATTTTGTTCATCATGCGGTGTTTTCATTTTCTG 768

RESULT 7
BI906283 876 bp mRNA linear EST 16-OCT-2001
LOCUS 603063222F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5212541 5',
DEFINITION mRNA sequence.
ACCESSION BI906283
VERSION BI906283.1 GI:16168946
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 876)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: L1A11533 row: k column: 06
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FEATURES High quality sequence stop: 800.
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    /clone="IMAGE:5212541"
    /tissue_type="leukocyte"
    /lab_host="DH10B"
    /clone_1lib="NIH_MGC_118"
    /note="Vector: pCMV-SPORT6, Site 1: NotI, Site 2: EcoRV
    (destroyed); RNA source leukocytes from anonymous pool of
    non-activated adult donors. Library is oligo-dT primed
    and directionally cloned (EcoRV site is destroyed upon
    cloning). Average insert size 1.7 kb, insert size range
    1.2-3.3 kb. Library is normalized and enriched for
    full-length clones and was constructed by C. Gruber
    (Invitrogen). Research Genetics tracking code 027. Note:
    this is a NIH_MGC Library."
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Query Match 66.1%; Score 703.8; DB 3; Length 876;
Best Local Similarity 97.2%; Pred. No. 3.4e-192;
Matches 769; Conservative 0; Mismatches 17; Indels 5; Gaps 5;
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QY 1 ATGACAACCTCACTAGATACAGTTGAGACCTTTGGTACCAATCCTACTATGATGACGTG 60
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Db 79 ATGACAACCTCACTAGATACAGTTGAGACCTTTGGTACCAATCCTACTATGATGACGTG 138
QY 61 GGCTGTCTGTGAAGAGCTGATACCAAGACATGATGCCCCAGTTGTGCCCGCTG 120
    |||||||
Db 139 GGCTGTCTGTGAAGAGCTGATACCAAGACATGATGCCCCAGTTGTGCCCGCTG 198
QY 121 TACTCCCTGTGTTCACTGTGGGCTCTTGGGCAATGTGTGTGATGATCTCTATA 180
    |||||||
Db 199 TACTCCCTGTGTTCACTGTGGGCTCTTGGGCAATGTGTGTGATGATCTCTATA 258
QY 181 AAATACAGAGGCTCCGAATTATGACCAACATCTACTGCTCAACCTGGCCATTTCGAC 240
    |||||||
Db 259 AAATACAGAGGCTCCGAATTATGACCAACATCTACTGCTCAACCTGGCCATTTCGAC 318
QY 241 CTGCTCTTCTCTGTCACCCCTTCCATTCTGGATCCACTATGTCAAGGGGCATACTGGGTT 300
    |||||||
Db 319 CTGCTCTTCTCTGTCACCCCTTCCATTCTGGATCCACTATGTCAAGGGGCATACTGGGTT 378
QY 301 TTGGCCATGCGCATGTGTAACTCTCTCAGGGTTTATCAGACAGGCTGTACAGCGAG 360
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Db 379 TTGGCCATGCGCATGTGTAACTCTCTCAGGGTTTATCAGACAGGCTGTACAGCGAG 438
QY 361 ATCTTTTTCATTAATCTGTCTGCAATCGACAGGTACCTGGCCATTGTCCATGTGTGTT 420
    |||||||
Db 439 ATCTTTTTCATTAATCTGTCTGCAATCGACAGGTACCTGGCCATTGTCCATGTGTGTT 498
QY 421 GCCCTTCGAGCCCGGACTGTCACTTTGGTGTATCACCAGCATCTGACCTGGGCGCTG 480
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Db 499 GCCCTTCGAGCCCGGACTGTCACTTATGTTGTATCACCAGCATCTGACCTGGGCGCTG 558
QY 481 GCAATGCTAGCAGCTCTTCTGAA-TTATCTTCTATGAGACTGAAGAGTTGTTGAAG 539
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Db 559 GCAATGCTAGCAGCTCTTCTGAACTTATCTTCTATGAGACTGAAGAG-TGTTGAAGA 617
QY 540 GACTCTTTGCAAGTGTCTTTTACCCAGAGATACAGTATATAGCTGAGGCAATTTCACAC 599
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Db 618 GACTCTTTGCAAGTGTCTTTTACCCAGAGATACAGTATATAGCTGAGGCAATTTCACAC 677
QY 600 TCTGAGAATGACCATCTTCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 658
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Db 678 TCTGAGAATGACCATCTTCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 737
QY 659 CAGGAATCATCAAAACGCTGTGAGGTGCCCCAGTAAAAAAAGTACA-AGGCCATCCGG 717
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Db 738 CAGGAATCATCAAAACGCTGTGAGGTGCCCCAGTAAAACAACAGTACAAGCCATCCGG 797
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Qy 718 CTCATTTTGTGTCATGCGGTGTTTTCATTTTCGACACCTACATGTCCTATC 777
Db 798 CTCATTTCCGCATCATGCGCGG-TAACCATTTTCTGACACCTACATGTCCTATC 856
Qy 778 CTTCCTCTCTTC 788
Db 857 CTTCCTCTATTC 867
RESULT 8
LOCUS CO960092 702 bp mRNA linear EST 17-AUG-2004
DEFINITION AGENCOURT_30842869 NIH_MGC_146 Homo sapiens cDNA clone
IMAGE:7389709 5', mRNA sequence.
ACCESSION CO960092
VERSION CO960092.1 GI:51324665
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 702)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: c9apbs-r@mail.nih.gov
Tissue Procurement: Guthrie cDNA Resource Center
cDNA Library Preparation: Guthrie cDNA Resource Center
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: IRB17 row: C column: 11
High quality sequence start: 26
High quality sequence stop: 538.
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/db_xref="taxon:9606"
/clone="IMAGE:7389709"
/tissue_type="mixed"
/lab_host="DH10B (TI-phage-resistant)"
/note="Vector: pCDNA3.1; Site 1: multiple; Site 2:
multiple; ORF's were PCR-amplified (from IMAGE clones or
from commercially available cDNA libraries) and cloned by
the Guthrie cDNA Resource Center (www.guthrie.org/cDNA)
into pCDNA3.1. For specific information on cloning sites
(which vary by clone), please refer to the Guthrie
website, using the Guthrie ID given in the file
ftp://image.lnl.gov/image.rearrayed_plates/IRBF.presv.dat
a. Note: this is a NIH_MGC Library."
ORIGIN
Query Match 64.0%; Score 681.4; DB 7; Length 702;
Best Local Similarity 98.4%; Pred. No. 9.7e-186;
Matches 688; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 1 ATGACAACTCACTAGATACAGTTGAGACCTTTGGTACCACTCCTATGATGACGTG 60
Db 3 ATGACAACTCACTAGATACAGTTGAGACCTTTGGTACCACTCCTATGATGACGTG 62
Qy 61 GGCTGCTCTGTGAAAAAGCTGATACAGACCACTGATGGCCCACTTGTGCCCCCGCTG 120
Db 63 GGCTGCTCTGTGAAAAAGCTGATACAGACCACTGATGGCCCACTTGTGCCCCCGCTG 122

Qy 121 TACTCCCTGCTGTCTCACTGTGGGCTCTTGGGCAATGTGGTGTGATGATCCTCAT 180
Db 123 TACTCCCTGCTGTCTCACTGTGGGCTCTTGGGCAATGTGGTGTGATGATCCTCAT 182
Qy 181 AATTAACAGAGGCTCCGAATTAAGACCAACATCTACCTGCTCAACCTGGCATTTCGAC 240
Db 183 AATTAACAGAGGCTCCGAATTAAGACCAACATCTACCTGCTCAACCTGGCATTTCGAC 242
Qy 241 CTGCTCTTCTCTGTCACCTTCCATTCTGATCCACTATGTGAGGGGCAATTACTGGGTT 300
Db 243 CTGCTCTTCTCTGTCACCTTCCATTCTGATCCACTATGTGAGGGGCAATTACTGGGTT 302
Qy 301 TTGGCCATGGCATGTGTAAAGCTCCTCTAGGGTTTATGACACAGGCTTGTACAGCGAG 360
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Db 363 ATCTTTTTCATTAATCCTGCTGACAAATCGACAGGTACCTGGCCATTGTCCATGCTGT 422
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Qy 481 GCAGTGTAGCAGCTCTTCTGAATTATCTTATGAGACTGAAGAGTGTGTTGAAGAG 540
Db 483 GCAGTGTAGCAGCTCTTCTGAATTATCTTATGAGACTGAAGAGTGTGTTGAAGAG 542
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Db 543 ACTCTTTCAGTGTCTCTTACCAGAGATACAGTATATAGCTGAGGCAATTTCCACT 602
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Db 603 CTGGAATGATACCATCTTGTGCTGCTTCTCCTCTGCTGCTTATGCGCATCTGCTTACCA 662
Qy 661 GGAATCATCAAAACGCTGCTGAGGTGCCCCAGTAAAAA 699
Db 663 GGAATCATTAACACGCTGCTGAGGTGCCAGTAAAAA 701

RESULT 9
LOCUS CV030237 675 bp mRNA linear EST 20-AUG-2004
DEFINITION 9286 Full Length cDNA from the Mammalian Gene Collection Homo
sapiens cDNA 5' similar to BC033514, mRNA sequence.
ACCESSION CV030237
VERSION CV030237.1 GI:5148473
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 675)
AUTHORS Rual,J.F., Hirozane-Kishikawa,T., Hao,T., Bertin,N., Li,S.,
Dricot,A., Li,N., Rosenberg,J., Lamesch,P., Vidalain,P.O.,
Clingingsmith,T.R., Hartley,J.L., Esposito,D., Cheo,D., Moore,T.,
Simmons,B., Sequerra,R., Bosak,S., Doucette-Stamm,L., Le Peuch,C.,
Vandenhaute,J., Cusick,M.E., Albala,J.S., Hill,D.B. and Vidal,M.
Human ORFeome Version 1.1: a Platform for Reverse Proteomics
Genome Res. (2004) In press
TITLE
JOURNAL
COMMENT Contact: Vidal M
Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739
Email: Marc_Vidal@dfci.harvard.edu
ORF Sequence Tag (OST) of Gateway Entry construct. Each cloned ORF
results from a PCR reaction using an MGC full-length cDNA as
template DNA and ORF specific primers
PCR Primers

FORWARD: ATGACAACCTCTACTAGATACAG
BACKWARD: TAAACACATAGAGGTTCCGC
Insert Length: 675 Std Error: 36.00
Plate: 11057 row: 03 column: E
Seq primer: ACTGGCCGTCGTTTACACGTCGTGACTGGGAAAC
High quality sequence start: 102
High quality sequence stop: 674
POLYA=No.

FEATURES
source location/Qualifiers

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/clone_lib="Full length cDNA from the Mammalian Gene
Collection"
/note="Vector: mixed; The ORFs were PCR amplified from the
MGC (Mammalian Gene Collection) as of April 2004 and
cloned by recombinational Gateway cloning into pDONR223
Donor vector. Reference : MGC (Mammalian Gene Collection)
Program Team, Generation and Initial Analysis of more than
15,000 Full-Length Human and Mouse cDNA Sequences. PNAS,
2002, 99(26), 16899-16903"

ORIGIN

Query Match 62.9%; Score 669.8; DB 7; Length 675;
Best Local Similarity 99.4%; Pred. No. 2.2e-182;
Matches 671; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ATGACAACCTCTACTAGATACAGTTGACCTTTGGTACCACATCTATGATGACGTG 60
Db 1 ATGACAACCTCTACTAGATACAGTTGACCTTTGGTACCACATCTATGATGACGTG 60
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Db 61 GGCCTGCTCTGTGAAAAAGCTGATACAGAGCACTGATGGCCCGATTGTGCCCGCTG 120
QY 121 TACTCCCTGCTGTTCACCTGTGGGCTCTTGGGCAATGTGGTGGTGTGATGATCCTCATA 180
Db 121 TACTCCCTGCTGTTCACCTGTGGGCTCTTGGGCAATGTGGTGGTGTGATGATCCTCATA 180
QY 181 AAATACAGAGGCTCCGAATTATGACCAACATCTACCTGCTCAACCTGGCCATTTCGGAC 240
Db 181 AAATACAGAGGCTCCGAATTATGACCAACATCTACCTGCTCAACCTGGCCATTTCGGAC 240
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QY 301 TTTGGCCATGGCATGTGTAAAGCTCTCTCAGGGTTTATCACACAGGCTTGTACAGCGAG 360
Db 301 TTTGGCCATGGCATGTGTAAAGCTCTCTCAGGGTTTATCACACAGGCTTGTACAGCGAG 360
QY 361 ATCTTTTCAATAATCTGCTGACCAATCGACAGGTACCTGGCCATTGTCATGCTGTGTTT 420
Db 361 ATCTTTTCAATAATCTGCTGACCAATCGACAGGTACCTGGCCATTGTCATGCTGTGTTT 420
QY 421 GCCCTCGAGCCCGGACTGTCACTTTTGGTGTCAATCACAGCATCGTCACTGGGCGCTG 480
Db 421 GCCCTCGAGCCCGGACTGTCACTTTTGGTGTCAATCACAGCATCGTCACTGGGCGCTG 480
QY 481 GCAGTGTACGACGCTTCTCCTGAATTATCTTCTATGAGACTGAAGAGTTGTTGAAGAG 540
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DEFINITION
AK041106 1761 bp mRNA linear HTC 03-APR-2004
Mus musculus adult male aorta and vein cDNA, RIKEN full-length
enriched library, clone:A530083H05 product:chemokine (C-C) receptor
3, full insert sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
AK041106 GI:26334210
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HTC; CAP trapper.
Mus musculus (house mouse)
Mus musculus
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
10349636

REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
11042159

REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsuina, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, B., Watabiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
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AUTHORS
TITLE
JOURNAL
PUBMED
The RIKEN Genome Exploration Research Group Phase II Team and the
PANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
5

REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
The PANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 1761)

REFERENCE
AUTHORS
TITLE
JOURNAL
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
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Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
Direct Submission

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
kanagawa 230-0045, Japan (E-mail:genome-res@sc.riken.jp,

COMMENT

URL: <http://genome.gsc.riken.jp/>, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL: <http://genome.gsc.riken.jp/>
URL: <http://fantom.gsc.riken.jp/>.

FEATURES

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OY 682 AGTGCCCCAGTAAAAAAAGTACAAGGCCATCCGCTCATTTTGTTCATCATGCGGCTG 741
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OY 802 TTATTTGAAATGACTGTGACCGGAGCAAGCATCTGACCTGTGATGCTGTGACAGAG 861
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RESULT 11
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LOCUS
DEFINITION Mus musculus activated spleen cDNA, RIKEN full-length enriched library, clone:F830035018 product:chemokine (C-C) receptor 3, full insert sequence.
ACCESSION AK089875 GI:26354710
VERSION AK089875.1
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Bukaryota; Metazoa; Chordata; Ctenophora; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
10349636
REFERENCE 2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
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11042159
REFERENCE 3
Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kishimoto, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,

TITLE
JOURNAL
PUBMED
11076861
4
The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
TITLE
JOURNAL
Nature 409, 685-690 (2001)
5
The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
TITLE
JOURNAL
Nature 420, 563-573 (2002)
6 (bases 1 to 2284)
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
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Kato,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
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Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
Muramatsu,M. and Hayashizaki,Y.
TITLE
JOURNAL
Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-res@gscl.riken.jp,
URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)
COMMENT
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
Trust/MRC building Addenbrookes Hospital Cambridge) whose
assistance we gratefully acknowledge.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
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Db 1268 GAGCAAGAAATCTCTGTGTGTTT 1291
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LOCUS
DEFINITION Mus musculus activated spleen cDNA, RIKEN full-length enriched library, clone:F830047J12 product:chemokine (C-C) receptor 3, full insert sequence.
ACCESSION AK089895
VERSION AK089895.1 GI:26354724
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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AUTHORS 1 Carninci,P. and Hayashizaki,Y.
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PUBMED 10349636
REFERENCE
AUTHORS 2 Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
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JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
PUBMED 11042159
REFERENCE
AUTHORS 3 Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Komno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Suni,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwaki,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,B., Watabiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
PUBMED 11076861
REFERENCE
AUTHORS 4 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
PUBMED 11076861
REFERENCE
AUTHORS 5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
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JOURNAL Nature 420, 563-573 (2002)
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REFERENCE
AUTHORS Adachi,J., Aizawa,K., Akiyama,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hirooka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohnato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,

TITLE
JOURNAL
Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gs.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.
URL:http://genome.gsc.riken.jp/
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Best Local Similarity 76.6%; Pred. No. 1.7e-177;
Matches 800; Conservative 0; Mismatches 244; Indels 0; Gaps 0;
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Db 119 GTTGAAGCTTGTGAGACCACACCTATGATATGAGTGGGACACACCTGTGAAAAAGTC 178
QY 82 GATACCAAGACATGATGGCCAGTTTGTGCCCCCGCTGTACTCCCTGTGTTCACTG 141
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Db 179 AGAATCAAGAGAGCTGGGTGATGGCTCTGCTCCACTGTACTCCCTGTGTTCACTG 238
QY 142 GGCCTCTTGGGCAATGTGGTGTGTGATGATCTCTATAAATAACAGAGGCTCCGAAT 201
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Db 239 GGCCTCTTGGGCAACATATGTGTGTGTGATCTCTATAAAGTACAGAGCTACAAT 298
QY 202 ATGACCAACATCTACCTGTCAACCTGGCCATTTGGACCTGCTCTCTGTCACTT 261
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Db 299 ATGGCTATATCTACCTGTCAACTTGGCAATTTGTGACCTGCTCTTCTTCACTGTC 358
QY 262 CCATTCTGATCCACTATGTCAAGGGGCAATACCTGGGTTTGGCCATGCGATGTAA 321
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Db 359 CCATTCTGATTCATATGTTCTGTGGAATGAGTGGGTTTGGCCACTACATGTGCAA 418

Oy		322	CTCCTCTCAGGGTTTATTCACACAGGCTTGTA CAGCGAATCTTTTCATAATCCTGCTG	381			
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Oy		382	ACAATGCACAGGTAACCTGGCCATTGTCCATGCTGTGTTGCCCTTCGAGCCCCGCACTGTC	441			
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Db		539	ACTTTTGTACTATCACAGATATCATTAACCTGGGCGCTGGCAAGACTGGCAATGCTCT	598			
Oy		502	GAATTTATCTTCTATAGA CTGAAGAGTTGTTGAAGAGACTCTTTGCAGTGTCTTTAC	561			
Db		599	GAATTTATCTTCCATGAGTCTCAAGACAGCTTTGAGAGTTTTCTCGAGTCCCTGGCTAT	658			
Oy		562	CCAGAGGATACAGTATATAGCTGGAAGGCATTTCCACATCTGAGATGACCATCTTCTGT	621			
Db		659	CCAGAGGGTGAAGAAAGACAGCTGGAAAACGTTTCCATGCTCTAAGATGATATCTTTGCT	718			
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Db		719	CTAGCTCTTCTCTCTCTCATTTATGGTTATCTGCTACTCAGGAATCATTAACCTCTCTG	778			
Oy		682	AGGTGCCCCAGTAAAAAAAGTACAAGGCCATCCGGCTCATTTTGTCAATGCGGCTG	741			
Db		779	AGATGTCCCAATAAAAAAACA CAAGGCCATCCGCTTAATTTTGTGTATGATAGTTC	838			
Oy		742	TTTTTCATTTTCTGGA CACCCTACAATGTGGCTATCCCTCTCTCTCTATCAATCCATC	801			
Db		839	TTTTTATTTTGTGGA CCCCCTACAACCTGGTCTCTTTTCTGCTTTTACAGCACA	898			
Oy		802	TTATTTGGAATGACTGTGA CGGAGCAAGCATCTGGAACCTGGTCACTGTGTGACAGAG	861			
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Oy		982	ATCCCATTCCTTCTTAGTGA AGAGCTGAAAAGAACCAAGCTCTGTCTCTCCATCCACAGCA	1041			
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VERSION	BG204024.1	GI:13725711					
KEYWORDS	EST.						
SOURCE	Homo sapiens (human)						
ORGANISM	Homo sapiens						
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;							
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;							
Homnidae; Homo.							
1 (bases 1 to 745)							
REFERENCE	Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,						
AUTHORS	Cain,S., Leventhal,C., Thornton,M., Ramachandran,R.,						
	Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Booser,S.,						
	Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K.,						
	Offenbacher,J., Danzig,J. and Ducar,M.						
Creation of genome-wide protein expression libraries using random							
TITLE							

JOURNAL activation of gene expression
 PUBMED Nat. Biotechnol. 19 (5), 440-445 (2001)
 11329013
 COMMENT Contact: Scott J. Cain
 Athersys, Inc.
 3201 Carnegie Ave, Cleveland, OH 44115, USA
 Tel: 216 431 9900
 Fax: 216 361 9596
 Email: scain@athersys.com
 High quality sequence stop: 447.
 location/Qualifiers
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 /cell_line="HT1080"
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 /note="See 'Creation of Genome-wide Protein Expression
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 Nature Biotechnology, in press. Note that even though the
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Query Match	61.2%;	Score 651.6;	DB 2;	Length 745;	
Best Local Similarity	95.7%;	Pred. No. 4.3e-177;			
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QY	130	GTGTTCACTGTGGGCTCTTGGGCAATGTGTGTGTGTAAGATCCTATAAATAACAGG	189		
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QY	250	CTCGTCAACCCCTTCCATTCTGATCCACTATGTCAAGGGGGCATACTGGGTTTGGCCAT	309		
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QY	370	ATAATCCTGCTGACAATCGACAGGTACCTGGCCATTGTCCATGCTGTGTTGCCCTTGA	429		
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QY	430	GCCCCGACTGTCACTTTTGGTGTCATCACCAAGCATGTCACCTGGGGCCTGGCAGTGCTA	489		
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QY	490	GCACTCTT - CCTGAATTATCTTATGAGACTGAAGAGTTGTTGAAGAGACTCTTTG	548		
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Db	736	CC	737
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AUTHORS			
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COMMENT			
FEATURES			
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gene			
ORIGIN			
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Best local Similarity			
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Qy	901	TACGCTTTGTTGAGAGAGGTTCCGGAATACCTGCGCCACTTCTTCCACAGGCACTTG	960
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Qy	961	CTCATGCACCTGGGCGAGTACATCCCATTTCTCTCTAGTGAAGCTGGAAGAACCAGC	1020
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ACCESSION CR609171			
VERSION CR609171.1 GI:50489978			
KEYWORDS HTC; CNSLT; cDNA.			
SOURCE Homo sapiens (human)			
ORGANISM Homo sapiens			
REFERENCE 1 (bases 1 to 2583)			
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.			
TITLE Full-length cDNA libraries and normalization			
JOURNAL Unpublished			
REMARK Contact : Peng Liang Email : fliang@lifetech.com URL :			

RESULT 15	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	REMARK
CR609171	CR609171	full-length cDNA clone CS0D1086YK11 of Placenta Cot 25-normalized of Homo sapiens (human) .	CR609171	CR609171.1	GI:50489978	HTC; CNSLT_CDNA.	Homo sapiens (human)	1 (bases 1 to 2583)	Li, W.B., Gruber, C., Jessee, J. and Polayes, D.	Full-length cDNA libraries and normalization	Unpublished	Contact : Feng Liang Email : fliang@lifetech.com URL : http://www.lifetech.com
							Homo sapiens					
							Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.					

http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paradise Avenue
2 (bases 1 to 2583)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.

COMMENT

Location/Qualifiers
1. 2583
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FEATURES

source

Query Match 50.8%; Score 540.8; DB 4; Length 2583;
Best Local Similarity 69.3%; Pred. No. 8.6e-145;
Matches 737; Conservative 0; Mismatches 327; Indels 0; Gaps 0;

ORIGIN

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19 ATGGAACTCCAAACACACACAGAGGATATGACACGACCAAGATTGACTATGGGGAT 78
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Search completed: January 7, 2006, 19:14:03
Job time : 3890.92 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 7, 2006, 07:05:07 ; Search time 83.4673 Seconds
(without alignments)
3912.475 Million cell updates/sec

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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4637609 segs, 364468668 residues

Total number of hits satisfying chosen parameters: 9275218

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 10: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	448	100.0	1915	7	US-11-068-686-3
2	448	100.0	1945	7	US-11-127-877-27
3	41	9.2	2908	6	US-10-793-626-4359
4	40.8	9.1	10467	6	US-10-240-708-2
5	40.4	9.0	6070	6	US-10-240-708-10
6	40.4	9.0	151169	7	US-11-121-086-38
7	40.2	9.0	151169	7	US-11-121-086-38
8	40	8.9	4765	6	US-10-750-185-64847
9	40	8.9	4765	6	US-10-750-623-64847
10	39	8.7	157230	7	US-11-112-908-64
11	39	8.7	166111	7	US-11-112-908-47
12	39	8.7	170508	7	US-11-112-908-62
13	39	8.7	173115	7	US-11-112-908-65
14	38.8	8.7	6306	6	US-10-240-708-49
15	37.6	8.4	201	6	US-10-995-561-60497
16	37.6	8.4	68123	6	US-10-995-561-13348
17	37.2	8.3	5278	6	US-10-750-185-61034
18	37.2	8.3	5278	6	US-10-750-623-61034
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C	27	36.8	8.2	1080000	6	US-10-928-446A-185	Sequence 185, App
C	28	36.8	8.2	1080000	6	US-10-928-446A-187	Sequence 187, App
C	29	36.8	8.2	1080000	6	US-10-928-446A-189	Sequence 189, App
C	30	36.8	8.2	1080000	6	US-10-928-446A-191	Sequence 191, App
C	31	36.8	8.2	1080000	6	US-10-928-446A-193	Sequence 193, App
C	32	36.8	8.2	1080000	6	US-10-928-446A-195	Sequence 195, App
C	33	36.8	8.2	1080000	6	US-10-928-446A-197	Sequence 197, App
C	34	36.8	8.2	1080000	6	US-10-928-446A-199	Sequence 199, App
C	35	36.8	8.2	1080000	6	US-10-928-446A-201	Sequence 201, App
	36	36.6	8.2	207908	7	US-11-112-908-21	Sequence 21, Appl
	37	36.6	8.2	212805	7	US-11-112-908-19	Sequence 19, Appl
	38	36.6	8.2	1082144	7	US-11-117-187-211	Sequence 211, App
	39	36.4	8.1	2286	6	US-10-750-185-60490	Sequence 60490, A
C	40	36.4	8.1	2286	6	US-10-750-623-60490	Sequence 60490, A
C	41	36.4	8.1	48000	7	US-11-159-597-20	Sequence 20, Appl
C	42	36.2	8.1	5152	6	US-10-240-708-73	Sequence 73, Appl
C	43	36.2	8.1	110711	6	US-10-995-561-13264	Sequence 13264, A
C	44	36	8.0	175416	7	US-11-121-086-43	Sequence 43, Appl
	45	35.8	8.0	1691140	7	US-11-091-018-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-11-068-686-3
; Sequence 3, Application US/11068686
; Publication NO. US20050260565A1
; GENERAL INFORMATION:
; APPLICANT: Gray, Patrick W.
; ; Schweickart, Vicky L.
; ; Raport, Carol J.
; ; TITLE OF INVENTION: Chemokine Receptor Materials and Methods
; ; NUMBER OF SEQUENCES: 20
; ; CORRESPONDENCE ADDRESSES:
; ; ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
; ; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; ; CITY: Chicago
; ; STATE: Illinois
; ; COUNTRY: USA
; ; ZIP: 60606
; ; COMPUTER READABLE FORM:
; ; MEDIUM TYPE: Floppy disk
; ; COMPUTER: IBM PC compatible
; ; OPERATING SYSTEM: PC-DOS/MS-DOS
; ; SOFTWARE: Patent in Release #1.0, Version #1.30
; ; CURRENT APPLICATION DATA:
; ; APPLICATION NUMBER: US/11/068, 686
; ; FILING DATE: 28-Feb-2005
; ; CLASSIFICATION: <Unknown>
; ; ATTORNEY/AGENT INFORMATION:
; ; NAME: Noland, Greta B.
; ; REGISTRATION NUMBER: 35,302
; ; REFERENCE/DOCKET NUMBER: 27866/33670
; ; TELECOMMUNICATION INFORMATION:
; ; TELEPHONE: 312-474-6300
; ; TELEFAX: 312-474-0448
; ; INFORMATION FOR SEQ ID NO: 3:
; ; SEQUENCE CHARACTERISTICS:
; ; LENGTH: 1915 base pairs
; ; TYPE: nucleic acid
; ; STRANDEDNESS: single
; ; TOPOLOGY: linear
; ; MOLECULE TYPE: CDNA
; ; FEATURS:
; ; NAME/KEY: CDS
; ; LOCATION: 362..1426
; ; FEATURS:
; ; NAME/KEY: misc feature
; ; OTHER INFORMATION: /= "88-2B polynucleotide and amino acid
; ;


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; Sequence 2, Application US/10240708
; Publication No. US20050282157A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
; FILE REFERENCE: 5013.1012
; CURRENT APPLICATION NUMBER: US/10/240,708
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: PCT/EP01/03971
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 2
; LENGTH: 10467
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-240-708-2
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Query Match          9.1%; Score 40.8; DB 6; Length 10467;
Best Local Similarity 59.5%; Pred. No. 0.83;
Matches 69; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
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QY      317 TAAAACTTTTATATTTTACATTAACCTTCAGCCAGCTATGTATATAATAAACAATT 376
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      3783 TTAACATTATATATATTCCTAAATATATCCCAATAAATACAAATTAATATACACATTT 3724

QY      377 TCACACAATACATAAGTTAACTATTTTCTAATGTGCTAGTCTTCCCT 432
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      3723 TAAAAAATAAATAACTAACCGAAGCTAATACTACATACCTAATATCCCAACT 3668
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RESULT 5
US-10-240-708-10/c
; Sequence 10, Application US/10240708
; Publication No. US20050282157A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
; TITLE OF INVENTION: by Assessing DNA Methylation
; FILE REFERENCE: 5013.1012
; CURRENT APPLICATION NUMBER: US/10/240,708
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: PCT/EP01/03971
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 10
; LENGTH: 6070
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
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US-10-240-708-10
Query Match          9.0%; Score 40.4; DB 6; Length 6070;
Best Local Similarity 51.1%; Pred. No. 0.86;
Matches 95; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

QY      207 ACTCATCATCAACCCCTAAAGCAGAGCTTGTCTCTCTCTAAATGAGTTACCTACA 266
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      2774 AATTATAATCTTTCTAAATATCTCATTCATTAAATAAATTAATAAATCTTAACATTTA 2715

QY      267 TTTTAATGCACCTGAATGTTAGATAGTACTATATATGCCCTACAAAAGGTAACCTTTT 326
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      2714 TTTTATATCTATATTTAATTAATTAATAATTAATTTCTTCAACAATATATACAAATTATA 2655

QY      327 TATATTTTATACATTAACTTCAGCCAGCTATTGATATAAATAAACAATTTTCACACAATA 386
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      2654 TAAATTAACCTACAATTATCTATTCATCTATTAATAAACAATCTAAATTTTCCCTTAA 2595

QY      387 CAATPA 392
      |||||
Db      2594 CTATTA 2589
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RESULT 6
US-11-121-086-38
; Sequence 38, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 38
; LENGTH: 151169
; TYPE: DNA
; ORGANISM: Homo sapiens
; OTHER INFORMATION:
US-11-121-086-38
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Query Match          9.0%; Score 40.4; DB 7; Length 151169;
Best Local Similarity 53.9%; Pred. No. 2.8;
Matches 83; Conservative 0; Mismatches 71; Indels 0; Gaps 0;
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QY      243 TCTCTCTAAATGAGTTACCTACATTTTAATGACCTGAAATGTAGATAGTACTATATG 302
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      47401 TATATATTAATATATAATATATATATTTATATTCATATATATATATATATTTATAT 47460

QY      303 CCGCTACAAAAGGTAAGCTTTTATATTTTATACATTAACCTTCAGCCAGCTATTTGATA 362
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      47461 ATATTATATATATTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATA 47520

QY      363 TAAATAAACATTTTCACACAATACATAAGTTA 396
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      47521 TAAATATATACTATATATATAATATAATATATATA 47554
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RESULT 7
US-11-121-086-38/c
; Sequence 38, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
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; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 38
; LENGTH: 151169
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-11-121-086-38

Query Match 9.0%; Score 40.2; DB 7; Length 151169;
Best Local Similarity 53.9%; Pred. No. 3.1;
Matches 104; Conservative 0; Mismatches 88; Indels 1; Gaps 1;

QY 230 AGAGCTTGTCTCTCTCTAAATGAGTTACCTACATTTAATGCACCTGAATGTAGA 289
DB 47555 ATATATATATTATTATATTATAGTATATATTATATATAATATATATTATATATTATA 47496
QY 290 TAGTACTATATGCGCTACAAAAGGTAAACTTTTATATTTTATACATTAACTTCAG 349
DB 47495 TATATAATATATAATAATAATATAATATAATATAATAATAATAATAATAATAATA 47436
QY 350 CCAGCTATTGATATAATAA-AAACATTTTCACACATACAAATTAAGTTAACTATTATT 408
DB 47435 ATGAATATAAATATATATATTATTATATATATAATAATATTAATTATGTATATTAT 47376
QY 409 TCTAATGTGCTA 421
DB 47375 ATTTATATATATA 47363

RESULT 8

US-10-750-185-64847/c
; Sequence 64847, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64847
; LENGTH: 4765
; TYPE: DNA
; ORGANISM: Bovine 19866880468220
; US-10-750-185-64847

Query Match 8.9%; Score 40; DB 6; Length 4765;
Best Local Similarity 54.9%; Pred. No. 1;
Matches 79; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 225 AAAGCAGAGCTTGTCTCTCTCTAAATGAGTTACCTACATTTAATGCACCTGAATG 284
DB 4652 AAAACATTTTGTCTCTCTGATAAAGTAGCTCACATTAACCTTAAGTAGAATG 4593
QY 285 TTAAGATAGTTACTATATGCGCTACAAAAGGTAAACTTTTATATTTTATACATTAAAC 344
DB 4592 TCCCATTTCTAATATATATGCGGAGTCATGTATATCTGTAATAACATAGTAATTTTC 4533
QY 345 TTCAGCCAGCTATTGATATAATA 368
DB 4532 TTTCACATATTTTATATAATAATA 4509

RESULT 9

US-10-750-623-64847/c
; Sequence 64847, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64847
; LENGTH: 4765
; TYPE: DNA
; ORGANISM: Bovine 19866880468220
; US-10-750-623-64847

Query Match 8.9%; Score 40; DB 6; Length 4765;
Best Local Similarity 54.9%; Pred. No. 1;
Matches 79; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 225 AAAGCAGAGCTTGTCTCTCTCTCTAAATGAGTTACCTACATTTAATGCACCTGAATG 284
DB 4652 AAAACATTTTGTCTCTCTGATAAAGTAGCTCACATTAACCTTAAGTAGAATG 4593
QY 285 TTAAGATAGTTACTATATGCGCTACAAAAGGTAAACTTTTATATTTTATACATTAAAC 344
DB 4592 TCCCATTTCTAATATATATGCGGAGTCATGTATATCTGTAATAACATAGTAATTTTC 4533
QY 345 TTCAGCCAGCTATTGATATAATA 368
DB 4532 TTTCACATATTTTATATAATAATA 4509

RESULT 10

US-11-112-908-64/c
; Sequence 64, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; APPLICANT: Davis, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112,908
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 64
; LENGTH: 157230
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-11-112-908-64

Query Match 8.7%; Score 39; DB 7; Length 157230;
Best Local Similarity 54.5%; Pred. No. 6.4;
Matches 78; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

Qy	280	GAATGTTAGATAGTTACTATATATGCCGCTACAAAAAGSTAAAACTTTATATTATATACA	339
Db	125173	GAAGTTCAGGTTATTAACATACCTGAAGAGTCAGTGAATTTAAATCTTTTAGACCTTAAAA	125114
Qy	340	TTAAGCTTCAGCCAGCTATTGATATAATTAACAATTTTCACACAATACATAAGTTAACT	399
Db	125113	TTACATTTGGACCAACCAACAAGATGAGAGAAAATATTTGCCAACTAAATATTAGTTAAT	125054
Qy	400	ATTTTATTTTCTAATGTGCTTAG	422
Db	125053	ATTTAATTTAAGAAATTAAGGCAAG	125031

RESULT 11
US-11-112-908-47

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; Sequence 47, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; APPLICANT: Davis, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112,908
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 47
; LENGTH: 166111
;
; TYPE: DNA
; ORGANISM: Homo sapiens
;
US-11-112-908-47

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Query Match	8.7%	Score 39;	DB 7;	Length 16611;
Best Local Similarity	48.8%	Pred. No. 6.5;		
Matches 105; Conservative	0;	Mismatches 110;	Indels 0;	Gaps 0;

[illegible]

RESULT 12
US-11-112-908-62/c
; Sequence 62, Application US/11112908
; Publication No. US20050260659A1

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; APPLICANT: Harris, Cole
; APPLICANT: Davis, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112,908
; CURRENT FILING DATE: 2005-04-22

```

```

; PRIOR APPLICATION NUMBER: US 60/564,758 .
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 62
;   LENGTH: 170508
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-112-908-62

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US-11-112-908-62

Query Match	8.7%	Score 39	DB 7	Length 170508
Best Local Similarity	54.5%	Pred. No. 6.6		
Matches 78	Conservative 0	Mismatches 65	Indels 0	Gaps 0
QY	280	GAATGTTAGATAGTTACTATATGCGGCTACAAAAGGTAACCTTTTATATTTATACA	339	
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QY	340	TTAAGTTTCAGCCAGCCTATGATATATAATAAACAATTTTCACACAATACATAAGTTAACT	399	
Db	108869	TTACATTGGACAACAACCAACAATGAGAGAAATAATTGCAAACTAATAATTAGTTTAAT	108810	
QY	400	ATTTATTTTCTAATGTGCTAG	422	
Db	108809	ATTTAATTTAAGAAATTAAGGCAAG	108787	

RESULT 13

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US-11-112-908-65/c
; Sequence 65, Application US/11112908
; Publication NO. US20050260659A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; APPLICANT: Davis, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112,908
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 65
; LENGTH: 173115
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-65

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Query Match	8.7%	Score 39;	DB 7;	Length 173115;
Best Local Similarity	54.5%	Pred. No. 6.6;		
Matches 78;	Conservative 0;	Mismatches 65;	Indels 0;	Gaps 0;

[illegible]

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OM nucleic - nucleic search, using sw model

Run on: January 7, 2006, 06:18:20 ; Search time 325.171 Seconds
(without alignments)
11393.018 Million cell updates/sec

Title: US-10-767-521-4

Perfect score: 448

Sequence: 1 taggtcagatgcagaaatt.....ccctgttaataaagcct 448

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Gapop 10_0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA Main:*

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- 2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
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- 8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	448	100.0	448	3	US-09-922-895-4 Sequence 4, Appl1
2	448	100.0	448	8	US-10-767-521-4 Sequence 4, Appl1
3	448	100.0	1717	3	US-09-964-824A-100 Sequence 100, App
4	448	100.0	1717	7	US-10-641-643-959 Sequence 959, App
5	448	100.0	1717	9	US-10-843-641A-5403 Sequence 5403, App
6	448	100.0	1915	5	US-10-106-623-3 Sequence 3, Appl1
7	448	100.0	1915	8	US-10-772-037-3 Sequence 3, Appl1
8	448	100.0	5791	9	US-10-929-182-21 Sequence 21, Appl1
9	448	100.0	5791	9	US-10-486-471-5 Sequence 5, Appl1
10	380.4	84.9	1689	3	US-09-931-381A-15 Sequence 15, Appl1
11	380.4	84.9	1689	6	US-10-283-028-1 Sequence 1, Appl1
12	339.2	75.7	7201	6	US-10-311-455-310 Sequence 310, App
13	294.4	65.7	7201	6	US-10-311-455-309 Sequence 309, App
14	105	23.4	600	10	US-11-060-756-2216 Sequence 2216, App
15	105	23.4	600	10	US-11-060-756-6488 Sequence 6488, App
16	105	23.4	1201	5	US-10-225-567A-63 Sequence 63, Appl1
17	105	23.4	1201	6	US-10-305-720-1085 Sequence 1085, App
18	105	23.4	1201	7	US-10-641-643-905 Sequence 905, App
19	105	23.4	1201	9	US-10-988-267-5 Sequence 5, Appl1
20	50	11.2	50	6	US-10-131-827-2200 Sequence 2200, App
21	48.4	10.8	3673778	6	US-10-312-841-2 Sequence 2, Appl1
22	46.8	10.4	7025	7	US-10-257-166-142 Sequence 142, App
23	46.8	10.4	7025	7	US-10-240-454-46 Sequence 46, Appl1

C	24	45.4	10.1	3673778	6	US-10-312-841-1	Sequence 1, Appl1
C	25	44	9.8	731	4	US-09-925-065A-934088	Sequence 934088,
C	26	43	9.6	650	5	US-10-027-632-231715	Sequence 231715,
C	27	43	9.6	650	5	US-10-027-632-231716	Sequence 231716,
C	28	43	9.6	650	5	US-10-027-632-231717	Sequence 231717,
C	29	43	9.6	650	6	US-10-027-632-231715	Sequence 231715,
C	30	43	9.6	650	6	US-10-027-632-231716	Sequence 231716,
C	31	43	9.6	650	6	US-10-027-632-231717	Sequence 231717,
C	32	43	9.6	3025	5	US-10-027-632-258968	Sequence 258968,
C	33	43	9.6	3025	5	US-10-027-632-258970	Sequence 258970,
C	34	43	9.6	3025	5	US-10-027-632-258971	Sequence 258971,
C	35	43	9.6	3025	6	US-10-027-632-258968	Sequence 258968,
C	36	43	9.6	3025	6	US-10-027-632-258970	Sequence 258970,
C	37	43	9.6	3025	6	US-10-027-632-258971	Sequence 258971,
C	38	42.8	9.6	731	4	US-09-925-065A-934087	Sequence 934087,
C	39	42.8	9.6	731	4	US-09-925-065A-934089	Sequence 934089,
C	40	42.6	9.5	3025	5	US-10-027-632-258969	Sequence 258969,
C	41	42.6	9.5	3025	6	US-10-027-632-258969	Sequence 258969,
C	42	42.2	9.4	2865	7	US-10-221-714A-42	Sequence 42, Appl1
C	43	42.2	9.4	5269	6	US-10-311-455-2029	Sequence 2029, App
C	44	42.2	9.4	9905	6	US-10-311-455-36	Sequence 36, Appl1
C	45	42	9.4	595	4	US-09-925-065A-605996	Sequence 605996,

ALIGNMENTS

RESULT 1
US-09-922-895-4
Sequence 4, Application US/09922895
Publication No. US20020192214A1

GENERAL INFORMATION:

APPLICANT: DAUGHERTY, BRUCE L.
DEMARTINO, JULIE A.
SICILIANO, SALVATORE J.
SPRINGER, MARTIN J.

TITLE OF INVENTION: EOSINOPHIL EOTAXIN RECEPTOR

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSER: Merck & Co., Inc.
STREET: P.O. Box 2000, 126 E. Lincoln Ave.

CITY: Rahway

STATE: NJ

COUNTRY: USA

ZIP: 07065-0900

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/922,895

FILING DATE: 06-Aug-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/847,296

FILING DATE: <Unknown>

APPLICATION NUMBER: 60/017,113

FILING DATE: 26-APR-1996

ATTORNEY/AGENT INFORMATION:

NAME: Thies, J. Eric

REGISTRATION NUMBER: 35,382

REFERENCE/DOCKET NUMBER: 19634Y

TELECOMMUNICATION INFORMATION:

TELEPHONE: 908-594-3904

TELEFAX: 908-594-4720

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 448 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

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; MOLECULE TYPE: CDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-922-895-4

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Query Match	100.0%;	Score 448;	DB 3;	Length 448;
Best Local Similarity	100.0%;	Pred. No. 4.5e-100;		
Matches 448;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

OY		1	TAGGTCAGATGCAGAAAATTGCCCTAAAGAGAAGGAACCAAGGAGATGAAGCAAACAATT	60
Dp		1	TAGGTCAGATGCAGAAAATTGCCCTAAAGAGAAGGAACCAAGGAGATGAAGCAAACAATT	60
OY		61	AAGCCTTCCACACTCACCTCTAAAAACAGTCTTCAAACTTCCAGTGCAACTGAAAGCTC	120
Dp		61	AAGCCTTCCACACTCACCTCTAAAAACAGTCTTCAAACTTCCAGTGCAACTGAAAGCTC	120
OY		121	TGGAAGACACTGAAATATACACACAGCAGTAGCAGTAGATGCATGACCCTAAGSTCATTT	180
Dp		121	TGGAAGACACTGAAATATACACACAGCAGTAGCAGTAGATGCATGACCCTAAGSTCATTT	180
OY		181	ACCA CAGGCCAGGGGCTGGCAGCGTACTCATCAACCCCTAAAAAGCAGACTTTGGCT	240
Dp		181	ACCA CAGGCCAGGGGCTGGCAGCGTACTCATCAACCCCTAAAAAGCAGACTTTGGCT	240
OY		241	TCTCTCTTAATAATGAGTTACCTACATTTTAATGCACTGATGTTAGATAGTACTATATA	300
Dp		241	TCTCTCTCTAAATGAGTTACCTACATTTTAATGCACTGATGTTAGATAGTACTATATA	300
OY		301	TGCCGCTACAAAAAGGTAAAACTTTTATATTTTATACATTAACTTCAGCCAGCTATTGA	360
Dp		301	TGCCGCTACAAAAAGGTAAAACTTTTATATTTTATACATTAACTTCAGCCAGCTATTGA	360
OY		361	TATATAATAAAAACATTTTACACACAATACAATPAGTTAACTATTATTCTPATGTGCTCT	420
Dp		361	TATATAATAAAAACATTTTACACACAATACAATPAGTTAACTATTATTCTPATGTGCTCT	420
OY		421	AGTTCCTTCCCTGCTTAATGAAAAGCTT	448
Dp		421	AGTTCCTTCCCTGCTTAATGAAAAGCTT	448

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RESULT 2
US-10-767-521-4
; Sequence 4, Application US/10767521
; Publication NO. US20050033024A1
; GENERAL INFORMATION:
; APPLICANT: DAUGHERTY, BRUCE L.
; APPLICANT: DEMARTINO, JULIE A.
; APPLICANT: SICILIANO, SALVATORE J.
; APPLICANT: SPRINGER, MARTIN J.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING EOSINOPHIL EOTAXIN
; TITLE OF INVENTION: RECEPTOR
; FILE REFERENCE: 19634YDACA
; CURRENT APPLICATION NUMBER: US/10/767,521
; CURRENT FILING DATE: 2004-01-29
; PRIOR APPLICATION NUMBER: 60/016,158
; PRIOR FILING DATE: 1996-04-26
; PRIOR APPLICATION NUMBER: 09/922,895
; PRIOR FILING DATE: 2001-09-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 448
; TYPE: DNA
; ORGANISM: Human
US-10-767-521-4

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Query Match	100.0%;	Score 448;	DB 8;	Length 448;
Best Local Similarity	100.0%;	Pred. No. 4.5e-100;		
Matches 448; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 1 TAGGTGAGATGCAGAAAATTGCCTTAAGAGAGGAAGCAACCAAGAGATGAGCAAACACATT 60

Db	1	TAGTCAGATGCAGAAATTTGCCATAAGAGAAAGACCAGAGATGAAGCAACACATT	60
Qy	61	AAGCCTTCCACACTCACCTCTAAAACAGTCTTCAAACCTCCAGTGCACACTGAAGCTC	120
Db	61	AAGCCTTCCACACTCACCTCTAAAACAGTCTTCAAACCTCCAGTGCACACTGAAGCTC	120
Qy	121	TTGAAGACACTGAATATATACACACAGCAGTAGCAGTAGATGATGACCTTAAGTCAAT	180
Db	121	TTGAAGACACTGAATATATACACACAGCAGTAGCAGTAGATGATGACCTTAAGTCAAT	180
Qy	181	ACCACAGGCCAGGGGCTGGGCGAGCGTACTCATCATCAACCTAAAAAGCAGAGCTTGGCT	240
Db	181	ACCACAGGCCAGGGGCTGGGCGAGCGTACTCATCATCAACCTAAAAAGCAGAGCTTGGCT	240
Qy	241	TCTCTCTAAAAATGAGTTACCTACATTTTAATGCACCTGAATGTTAGATAGTTACTATA	300
Db	241	TCTCTCTAAAAATGAGTTACCTACATTTTAATGCACCTGAATGTTAGATAGTTACTATA	300
Qy	301	TGCGGCTACAAAAAGTAAAACTTTTATATTATTATACATTAACTTCAGCCAGCTATTGA	360
Db	301	TGCGGCTACAAAAAGTAAAACTTTTATATTATTATACATTAACTTCAGCCAGCTATTGA	360
Qy	361	TATAAATPAAAAATTTTTCACACAATACATAAGTTAACTATTTTATTTTCTAAATGTCCT	420
Db	361	TATAAATPAAAAATTTTTCACACAATACATAAGTTAACTATTTTATTTTCTAAATGTCCT	420
Qy	421	AGTTCTTCCCTGCTTAATGAAAAGCTT	448
Db	421	AGTTCTTCCCTGCTTAATGAAAAGCTT	448

RESULT 3
 US-09-964-824A-100
 ; Sequence 100, Application US/09964824A
 ; Patent No. US20020102531A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Horrigan, Stephen
 ; TITLE OF INVENTION: Cancer Gene Determinat
 ; TITLE OF INVENTION: Sets
 ; FILE REFERENCE: 689290-73
 ; CURRENT APPLICATION NUMBER: US/09/964, 824A
 ; CURRENT FILING DATE: 2001-09-27
 ; PRIOR APPLICATION NUMBER: US/60/236, 033
 ; PRIOR FILING DATE: 2000-09-28
 ; PRIOR APPLICATION NUMBER: US/60/236, 032
 ; PRIOR FILING DATE: 2000-09-28
 ; PRIOR APPLICATION NUMBER: US/60/236, 028
 ; PRIOR FILING DATE: 2000-09-28
 ; NUMBER OF SEQ ID NOS: 583
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 100
 ; LENGTH: 1717
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-964-824A-100

Query Match	100.0%;	Score 448;	DB 3;	Length 1717;
Best Local Similarity	100.0%;	Pred. No. 7.9e-100;		
Matches 448; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

QY	1	TAGTCAGATGCAGAAATTGCTTAAAGAGGAAGACCAGAGATGAAGCAACACATT	60
DB	1270	TAGTCAGATGCAGAAATTGCTTAAAGAGGAAGACCAGAGATGAAGCAACACATT	1329
QY	61	AAGCCTTCCACACTCACCTCTTAAACAGTCTTCAAACTTCAGTGCAACACTGAAGCTC	120
DB	1330	AAGCCTTCCACACTCACCTCTTAAACAGTCTTCAAACTTCAGTGCAACACTGAAGCTC	1389
QY	121	TTGAAGACACTGAATATATACACAGCAGTAGCAGTAGATGATGTACCCTTAAGGTCAATT	180
DB	1390	TTGAAGACACTGAATATATACACAGCAGTAGCAGTAGATGATGTACCCTTAAGGTCAATT	1449
QY	181	ACCACAGGCCAGGGGCTGGGCAAGCGTACTCATCATCAACCTTAAAAAAGCAGAGCTTTGCT	240


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Db 1450 ACCACAGGCCAGGGCTGGGCGAGGTACTCATCATCAACCCGTAAGGAGAGAGCTTGCT 1509
QY 241 TCTCTCTCTAAATGAGTTACCTACATTTTAATGACACCTGAATGTAGATAGTTACTATA 300
Db 1510 TCTCTCTCTAAATGAGTTACCTACATTTTAATGACACCTGAATGTAGATAGTTACTATA 1569
QY 301 TGGCGCTACAAAAGGTAAACTTTTATATTTTATACATTAATTGACCCAGCTATTGA 360
Db 1570 TGGCGCTACAAAAGGTAAACTTTTATATTTTATACATTAATTGACCCAGCTATTGA 1629
QY 361 TATAAATAAAACATTTTCACACATACATAAGTTAACTATTTTATTTCTAATGTGCT 420
Db 1630 TATAAATAAAACATTTTCACACATACATAAGTTAACTATTTTATTTCTAATGTGCT 1689
QY 421 AGTTCTTCCCTGCTTAATGAAAAGCTT 448
Db 1690 AGTTCTTCCCTGCTTAATGAAAAGCTT 1717
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RESULT 4

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US-10-641-643-959
; Sequence 959, Application US/10641643
; Publication No. US20040077003A1
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; Susan G. Stuart
; Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
; GENE EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/641,643
; FILING DATE: 14-Aug-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 959:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1717 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g1480480
; SEQUENCE DESCRIPTION: SEQ ID NO: 959 :
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Query Match 100.0%; Score 448; DB 7; Length 1717;
Best Local Similarity 100.0%; Pred. No. 7.9e-100;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 TAGGTCAAGTCAGAAAATTGCTTAAAGAGGAAGGACCAAGAGATGAAGCAACACATT 60
Db 1270 TAGGTCAAGTCAGAAAATTGCTTAAAGAGGAAGGACCAAGAGATGAAGCAACACATT 1329
QY 61 AAGCTTCCACACTCACCCTCTTAAAACAGTCCCTTCAAACTTCCAGTGCACACTGAAGCTC 120
Db 1330 AAGCTTCCACACTCACCCTCTTAAAACAGTCCCTTCAAACTTCCAGTGCACACTGAAGCTC 1389
QY 121 TTGAAGACACTGAATATATACACACAGAGTAGCAGTAGATGATGATACCCCTAAGGTCAAT 180
Db 1390 TTGAAGACACTGAATATATACACACAGAGTAGCAGTAGATGATGATACCCCTAAGGTCAAT 1449
QY 181 ACCACAGGCCAGGGCTGGGCGAGGTACTCATCATCAACCCGTAAGGAGAGAGCTTGCT 240
Db 1450 ACCACAGGCCAGGGCTGGGCGAGGTACTCATCATCAACCCGTAAGGAGAGAGCTTGCT 1509
QY 241 TCTCTCTCTAAATGAGTTACCTACATTTTAATGACACCTGAATGTAGATAGTTACTATA 300
Db 1510 TCTCTCTCTAAATGAGTTACCTACATTTTAATGACACCTGAATGTAGATAGTTACTATA 1569
QY 301 TGGCGCTACAAAAGGTAAACTTTTATATTTTATACATTAATTGACCCAGCTATTGA 360
Db 1570 TGGCGCTACAAAAGGTAAACTTTTATATTTTATACATTAATTGACCCAGCTATTGA 1629
QY 361 TATAAATAAAACATTTTCACACATACATAAGTTAACTATTTTATTTCTAATGTGCT 420
Db 1630 TATAAATAAAACATTTTCACACATACATAAGTTAACTATTTTATTTCTAATGTGCT 1689
QY 421 AGTTCTTCCCTGCTTAATGAAAAGCTT 448
Db 1690 AGTTCTTCCCTGCTTAATGAAAAGCTT 1717
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RESULT 5

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US-10-843-641A-5403
; Sequence 5403, Application US/10843641A
; Publication No. US20050064454A1
; GENERAL INFORMATION:
; APPLICANT: Avalon Pharmaceuticals, Inc.
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
; FILE REFERENCE: 689290-189
; CURRENT APPLICATION NUMBER: US/10/843,641A
; CURRENT FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: US/09/873,367
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US/09/954,531
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/09/954,456
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,436
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,832
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/964,824
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/09/967,768
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US/09/968,007
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,347
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,708
; PRIOR FILING DATE: 2001-10-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 8447
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5403
; LENGTH: 1717
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-843-641A-5403
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Query Match      100.0%; Score 448; DB 9; Length 1717;
Best Local Similarity 100.0%; Pred. No. 7.9e-100;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TAGTCAGATGCAGAAAATTGCTTAAAGAGAAGACCAAGATGAAGCAAAACACTT 60
        |||
DB      1270 TAGTCAGATGCAGAAAATTGCTTAAAGAGAAGACCAAGATGAAGCAAAACACTT 1329

QY      61 AAGCCTTCCACACTCACCTCTAAAACAGTCCTTCAAACCTTCAGTGCAACACTGAAGCTC 120
        |||
DB      1330 AAGCCTTCCACACTCACCTCTAAAACAGTCCTTCAAACCTTCAGTGCAACACTGAAGCTC 1389

QY      121 TTGAAGACACTGAATAATATACACACAGCAGTAGCAGTAGATGATGTACCCTAAGTCAAT 180
        |||
DB      1390 TTGAAGACACTGAATAATATACACACAGCAGTAGCAGTAGATGATGTACCCTAAGTCAAT 1449

QY      181 ACCACAGGCCAGGGGCTGGGCGACGCTACTCATCATCAACCTTAAAAAGCAGAGCTTTGCT 240
        |||
DB      1450 ACCACAGGCCAGGGGCTGGGCGACGCTACTCATCATCAACCTTAAAAAGCAGAGCTTTGCT 1509

QY      241 TCTCTCTCTAAAATGAGTTACCTACATTTTAATGCACCTGATGTAGATAGTTACTATA 300
        |||
DB      1510 TCTCTCTCTAAAATGAGTTACCTACATTTTAATGCACCTGATGTAGATAGTTACTATA 1569

QY      301 TGCCGCTACA AAAAGGTAAAACTTTTATATTTTATATATTAATTAACCTTCAGCCAGCTATTGA 360
        |||
DB      1570 TGCCGCTACA AAAAGGTAAAACTTTTATATTTTATATATTAATTAACCTTCAGCCAGCTATTGA 1629

QY      361 TATAAATAAACAATTTCACACAATACATAAAGTTAACPAATTTTATTTCTAATGTGCT 420
        |||
DB      1630 TATAAATAAACAATTTCACACAATACATAAAGTTAACPAATTTTATTTCTAATGTGCT 1689

QY      421 AGTTCTTTCCCTGCTTAATGA AAAAGCTT 448
        |||
DB      1690 AGTTCTTTCCCTGCTTAATGA AAAAGCTT 1717

RESULT 6
US-10-106-623-3
; Sequence 3, Application US/10106623
; Publication No. US20020150888A1
; GENERAL INFORMATION:
;   APPLICANT: Gray, Patrick W.
;             Schweickart, Vicki L.
;             Raport, Carol J.
; TITLE OF INVENTION: Chemokine Receptor Materials and Methods
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESSES:
;   ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
;   STREET: 6300 Sears Tower, 233 S. Wacker Drive
;   CITY: Chicago
;   STATE: Illinois
;   COUNTRY: USA
;   ZIP: 60606
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/10/106,623
;   FILING DATE: 26-Mar-2002
;   CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/771,276
;   FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
;   NAME: No. US20020150888A1and, Greta E.
;   REGISTRATION NUMBER: 35,302
;   REFERENCE/DOCKET NUMBER: 27866/33670
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 312-474-6300
;   TELEFAX: 312-474-0448

```

```

; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 1915 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 362..1426
; FEATURE:
;   NAME/KEY: misc feature
;   OTHER INFORMATION: /= "88-2B polynucleotide and amino acid
;   sequences"
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-106-623-3

Query Match      100.0%; Score 448; DB 5; Length 1915;
Best Local Similarity 100.0%; Pred. No. 8.3e-100;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TAGGTGAGATGAGAAAATTGCGTTAAAGAGAGAGCAAGAGATGAAGCAACACATT 60
      |||||||
Db      1427 TAGGTGAGATGAGAAAATTGCGTTAAAGAGAGAGCAAGAGATGAAGCAACACATT 1486

QY      61 AAGCCTTCCACACTCACTCTTAAACAGTCCCTCAAACTTCCAGTGCAACACTGAAGCTC 120
      |||||||
Db      1487 AAGCCTTCCACACTCACTCTTAAACAGTCCCTCAAACTTCCAGTGCAACACTGAAGCTC 1546

QY      121 TTGAAGACACTGAATATATACACACAGCAGTAGCAGTAGATGCATGTACCCTAAGTCATT 180
      |||||||
Db      1547 TTGAAGACACTGAATATATACACACAGCAGTAGCAGTAGATGCATGTACCCTAAGTCATT 1606

QY      181 ACCACAGGCCAGGGGCTGGGCGAGCGTACTCATCATCAACCCCTAAAAAGCAGAGCTTTGCT 240
      |||||||
Db      1607 ACCACAGGCCAGGGGCTGGGCGAGCGTACTCATCATCAACCCCTAAAAAGCAGAGCTTTGCT 1666

QY      241 TCTCTCTTAAATGAGTTACCTACATTTTAATGCACTGAATGTTAGATAGTTACTATA 300
      |||||||
Db      1667 TCTCTCTTAAATGAGTTACCTACATTTTAATGCACTGAATGTTAGATAGTTACTATA 1726

QY      301 TGCCGCTACAAAAAGGTAAAACTTTTATATTTTATATCAATTAACCTTCAGCCAGCTATTGA 360
      |||||||
Db      1727 TGCCGCTACAAAAAGGTAAAACTTTTATATTTTATATCAATTAACCTTCAGCCAGCTATTGA 1786

QY      361 TATAAATAAACAATTTTACACACATACATCAATAAAGTTAACTATTTTCTTAATGCGCT 420
      |||||||
Db      1787 TATAAATAAACAATTTTACACACATACATCAATAAAGTTAACTATTTTCTTAATGCGCT 1846

QY      421 AGTTCCTTCCCTGCTTAATGAAAAAGCTT 448
      |||||||
Db      1847 AGTTCCTTCCCTGCTTAATGAAAAAGCTT 1874

RESULT 7
US-10-772-037-3
; Sequence 3, Application US/10772037
; Publication No. US20040230037A1
; GENERAL INFORMATION:
;   APPLICANT: Gray, Patrick W.
;               Schweickart, Vicki L.
;               Raport, Carol J.
; TITLE OF INVENTION: Chemokine Receptor Materials and Methods
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borum
;   STREET: 6300 Sears Tower, 233 S. Wacker Drive
;   CITY: Chicago
;   STATE: Illinois
;   COUNTRY: USA
;   ZIP: 60606
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk

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: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.30
:
: CURRENT APPLICATION DATA:
:   APPLICATION NUMBER: US/10/772,037
:   FILING DATE: 04-Feb-2004
:   CLASSIFICATION: 435
:
: PRIOR APPLICATION DATA:
:   APPLICATION NUMBER: US/08/771,276
:   FILING DATE: 20-DEC-1996
:
: ATTORNEY/AGENT INFORMATION:
:   NAME: Noland, Greta E.
:   REGISTRATION NUMBER: 35,302
:   REFERENCE/DOCKET NUMBER: 27866/33670
:
: TELECOMMUNICATION INFORMATION:
:   TELEPHONE: 312-474-6300
:   TELEFAX: 312-474-0448
:
: INFORMATION FOR SEQ ID NO: 3:
:
:   SEQUENCE CHARACTERISTICS:
:     LENGTH: 1915 base pairs
:     TYPE: nucleic acid
:     STRANDEDNESS: single
:     TOPOLOGY: linear
:   MOLECULE TYPE: cDNA
:
:   FEATURE:
:     NAME/KEY: CDS
:     LOCATION: 362..1426
:
:   FEATURE:
:     NAME/KEY: misc feature
:     OTHER INFORMATION: /= "88-2B polynucleotide and amino acid
:       sequences"
:
:   SEQUENCE DESCRIPTION: SEQ ID NO: 3:

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Query Match	100.0%;	Score 448;	DB 8;	Length 1915;
Best Local Similarity	100.0%;	Pred. No. 8.3e-100;		
Matches 448;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy 1	TAGGTGAGATGCAGAAAAATTGGCTTAAGAAGGAGGAGCCAGAGATGATGAAGCAAAACACTT	60		
Db 1427	TAGGTGAGATGCAGAAAAATTGGCTTAAGAAGGAGGAGCCAGAGATGATGAAGCAAAACACTT	1486		
Qy 61	AAGCCTTCCACACTCACTCTAATAAACAGTCCCTTCAAACTTCCAGTGCACACTGAAGCTC	120		
Db 1487	AAGCCTTCCACACTCACTCTAATAAACAGTCCCTTCAAACTTCCAGTGCACACTGAAGCTC	1546		
Qy 121	TTGAAGACACTGAATAATATACACACAGCAGTAGCAGTAGATGATGTACCTTAAGGTCAAT	180		
Db 1547	TTGAAGACACTGAATAATATACACACAGCAGTAGCAGTAGATGATGTACCTTAAGGTCAAT	1606		
Qy 181	ACCACAGGCCAGGGGCTGGGCGAGCGTACTCATCATCAACCTTAATAAAGCAGAGCTTGGCT	240		
Db 1607	ACCACAGGCCAGGGGCTGGGCGAGCGTACTCATCATCAACCTTAATAAAGCAGAGCTTGGCT	1666		
Qy 241	TCTCTCTCTAAATGAGTTAACCCTACATTTTAAATGCACTGAATGTTAGATAGTTACTATA	300		
Db 1667	TCTCTCTCTAAATGAGTTAACCCTACATTTTAAATGCACTGAATGTTAGATAGTTACTATA	1726		
Qy 301	TGCCGCTACAAAAAGGTAAAACTTTTATATTTTATATACATTAACCTTCAGCCAGCTATTGA	360		
Db 1727	TGCCGCTACAAAAAGGTAAAACTTTTATATTTTATATACATTAACCTTCAGCCAGCTATTGA	1786		
Qy 361	TATAAATAAAAACATTTTCAACAATACAAATGAATTAACTTAATTTTCTTAATGTGCT	420		
Db 1787	TATAAATAAAAACATTTTCAACAATACAAATGAATTAACTTAATTTTCTTAATGTGCT	1846		
Qy 421	AGTTCCTTCCCTGCTTAATGAAAAAGCTT 448			
Db 1847	AGTTCCTTCCCTGCTTAATGAAAAAGCTT 1874			

RESULT 8
US-10-929-182-21

```

; Sequence 21, Application US/10929182
; Publication No. US20050064483A1
; GENERAL INFORMATION:
; APPLICANT: Zang, Jingwu
; APPLICANT: Hong, Jian
; TITLE OF INVENTION: Gene Expression Profiling Technology for Treatment Evaluation of
; TITLE OF INVENTION: Multiple Sclerosis
; FILE REFERENCE: HO-P02859US1
; CURRENT APPLICATION NUMBER: US/10/929,182
; CURRENT FILING DATE: 2004-08-30
; PRIOR APPLICATION NUMBER: US 60/498,731
; PRIOR FILING DATE: 2003-08-28
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 21
; LENGTH: 5791
; TYPE: DNA
; ORGANISM: HUMAN
US-10-929-182-21

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Query Match	100.0%;	Score 448;	DB 9;	Length 5791;
Best Local Similarity	100.0%;	Pred. No: 1.3e-99;		
Matches 448;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY 1	TAGTCAGATGCAGAAAATTGCTTAAAGAGGAGCAACCAAGAGATGAAGCAACACATT	60		
DB 5080	TAGTCAGATGCAGAAAATTGCTTAAAGAGGAGCAACCAAGAGATGAAGCAACACATT	5139		
QY 61	AAGCCTTCCACACTCACCTCTAAACAGTCTTCAACTTCCAGTCAACACTGAACTC	120		
DB 5140	AAGCCTTCCACACTCACCTCTAAACAGTCTTCAACTTCCAGTCAACACTGAACTC	5199		
QY 121	TTGAAGACACTGAAATATATACACACAGCAGTACGATGATGCATGTACCTTAAGTCAAT	180		
DB 5200	TTGAAGACACTGAAATATATACACACAGCAGTACGATGATGCATGTACCTTAAGTCAAT	5259		
QY 181	ACCACAGGCCAGGGGCTGGGCGAGCGTACTCATCAACCTTAAAAAGCAGAGCTTTGCT	240		
DB 5260	ACCACAGGCCAGGGGCTGGGCGAGCGTACTCATCAACCTTAAAAAGCAGAGCTTTGCT	5319		
QY 241	TCTCTCTCTAAAAATGAGTTACCTACATTTTAAATGCACTGAATGTTAGATACTACTATA	300		
DB 5320	TCTCTCTCTAAAAATGAGTTACCTACATTTTAAATGCACTGAATGTTAGATACTACTATA	5379		
QY 301	TGCCGCTACAAAAAGGTAAAACTTTTATATTTTATATCACTTAACCTCAGCCAGCTATTGA	360		
DB 5380	TGCCGCTACAAAAAGGTAAAACTTTTATATTTTATATCACTTAACCTCAGCCAGCTATTGA	5439		
QY 361	TATAAATAAAACATTTTACACACATACAAATAAGTTAACTATTATTCTAATGTGCTT	420		
DB 5440	TATAAATAAAACATTTTACACACATACAAATAAGTTAACTATTATTCTAATGTGCTT	5499		
QY 421	AGTTCCTTCCCTGCTTAATGAAGAAGCTT	448		
DB 5500	AGTTCCTTCCCTGCTTAATGAAGAAGCTT	5527		

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RESULT 9
US-10-486-471-5
; Sequence 5, Application US/10486471
; Publication No. US20050101530A1
; GENERAL INFORMATION:
; APPLICANT: TOPIGEN PHARMACEUTIQUE INC.
; TITLE OF INVENTION: CELLULAR VIRUS RECEPTORS AND METHODS OF USE
; FILE REFERENCE: 009953-0003
; CURRENT APPLICATION NUMBER: US/10/486,471
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: U.S. 60/311,088
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
;
; LENGTH: 5791
;

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/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (4015)..(5082)
/ OTHER INFORMATION:
/ PUBLICATION INFORMATION:
/ DATABASE ACCESSION NUMBER: GenBank AF247361
/ DATABASE ENTRY DATE: 2002-06-26
/ RELEVANT RESIDUES: (1)..(5791)
US-10-486-471-5

Query Match      100.0%; Score 448; DB 9; Length 5791;
Best Local Similarity 100.0%; Pred. No. 1.3e-99;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TAGGTCAGATGCAGAAATTCCTTAAAGAGGAGCAAGAGATGAAGCAACACATT 60
DB      5080 TAGGTCAGATGCAGAAATTCCTTAAAGAGGAGCAAGAGATGAAGCAACACATT 5139

QY      61 AAGCCTCCACACTCACCCTCTAATAACAGTCCTTCAAACTTCCAGTGCACACACTGAAGCTC 120
DB      5140 AAGCCTCCACACTCACCCTCTAATAACAGTCCTTCAAACTTCCAGTGCACACACTGAAGCTC 5199

QY      121 TTGAAGACACTGAAATATACACACAGCAGTAGCAGTAGATGATGATCCCTAAGGTCATT 180
DB      5200 TTGAAGACACTGAAATATACACACAGCAGTAGCAGTAGATGATGATCCCTAAGGTCATT 5259

QY      181 ACCACAGGCCAGGGGCTGGGAGCGTACTCATCATCAACCTTAAAAAAGCAGAGCTTGGCT 240
DB      5260 ACCACAGGCCAGGGGCTGGGAGCGTACTCATCATCAACCTTAAAAAAGCAGAGCTTGGCT 5319

QY      241 TCTCTCTCTAAATGAGTTACCTACATTTTATGACACCTGAATGTTAGATAGTACTATA 300
DB      5320 TCTCTCTCTAAATGAGTTACCTACATTTTATGACACCTGAATGTTAGATAGTACTATA 5379

QY      301 TGGCGCTACAAAAAGGTAAACCTTTTATATTATATACATTAACCTTCAGCCAGCTATTGA 360
DB      5380 TGGCGCTACAAAAAGGTAAACCTTTTATATTATATACATTAACCTTCAGCCAGCTATTGA 5439

QY      361 TATTAATAATAAACATTTTACACACAATACATAAGTTAACTATTATTCTTAATGTGCT 420
DB      5440 TATTAATAATAAACATTTTACACACAATACATAAGTTAACTATTATTCTTAATGTGCT 5499

QY      421 AGTTCTTCCCTGCTTAATGAAAAGCTT 448
DB      5500 AGTTCTTCCCTGCTTAATGAAAAGCTT 5527

RESULT 10
US-09-931-381A-15
/ Sequence 15, Application US/09931381A
/ Patent No. US20020137107A1
/ GENERAL INFORMATION:
/ APPLICANT: Butcher, Eugene C.
/ APPLICANT: Kunkel, Eric J.
/ APPLICANT: Pan, Junliang
/ APPLICANT: Soler-Ferran, Dulce
/ TITLE OF INVENTION: Method for Identifying Agents Which
/ TITLE OF INVENTION: Modulate Chemokine "MCC"-Induced Functions of CCR3 and/or
/ TITLE OF INVENTION: CCR10
/ FILE REFERENCE: 1855.2010-003
/ CURRENT APPLICATION NUMBER: US/09/931,381A
/ PRIOR FILING DATE: 2001-08-15
/ PRIOR APPLICATION NUMBER: U.S. 09/638,914
/ NUMBER OF SEQ ID NOS: 24
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 15
/ LENGTH: 1689
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
```

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/ NAME/KEY: CDS
/ LOCATION: (181)...(1248)
/ NAME/KEY: misc feature
/ LOCATION: (1291)...(1291)
/ OTHER INFORMATION: n = A, T, C or G
US-09-931-381A-15

Query Match      84.9%; Score 380.4; DB 3; Length 1689;
Best Local Similarity 98.4%; Pred. No. 3.4e-83;
Matches 436; Conservative 0; Mismatches 2; Indels 5; Gaps 5;

QY      7 AGATGCAGAAATTCCTTAAAGAGGAGCAAGAGATGAAGCAACACATTAGCCT 66
DB      1251 AGATGCAGAAATTCCTTAAAGAGGAGCAAGAGATGAAGCAACACATTAGCCT 1310

QY      67 TCCCACTCACCCTCTAATAACAGTCCTTCAA-CTTCCAGTGCAACACTGAAGCTTGA 125
DB      1311 TCCCACTCACCCTCTAATAACAGTCCTTCAAACCTTCCAGTGCAACACTGAAGCTT-AA 1369

QY      126 GACACTGAAATATACACACAGCAGTAGCAGTAGATGATGATACCCTAAGTCATTACCA 185
DB      1370 GACACTGAAATATACACACAGCAGTAGCAGTAGATGATGATACCCTAAGTCATTACCA 1429

QY      186 AGGCCAGGGGCTGGGAGCGTACTCATCATCAACCTTAAAAAAGCAGAGCTTGGCTCT 245
DB      1430 AGGCCA-GGGCTGGGAGCGTACTCATCATCA-CTTAAAAAAGCAGAGCTTGGCTCTCT 1487

QY      246 CTCTAAATGAGTTACCTACATTTTATGACACCTGAATGTTAGATAGTACTATATGCCG 305
DB      1488 CTCTAAATGAGTTACCTACATTTTATGACACCTGAATGTTAGATAGTACTATATGCCG 1547

QY      306 CTACAAAAAGGTAAACCTTTTATATTATACATTAACTTCAGCCAGCTATTGATATAA 365
DB      1548 CTACAAAAAGGTAAACCTTTTATATTATATTTATACATTAACTTCAGCCAGCTATT-ATAATA 1606

QY      366 ATTAACAATTTTACACACAATACATAAGTTAACTATTATTCTAATGTGCCATGTC 425
DB      1607 ATTAACAATTTTACACACAATACATAAGTTAACTATTATTCTAATGTGCCATGTC 1666

QY      426 TTCCCTGCTTAATGAAAAGCTT 448
DB      1667 TTCCCTGCTTAATGAAAAGCTT 1689

RESULT 11
US-10-283-028-1
/ Sequence 1, Application US/10283028
/ Publication No. US20030143684A1
/ GENERAL INFORMATION:
/ APPLICANT: Gerard, Craig J.
/ Gerard, No. US20030143684A1ma P.
/ Mackay, Charles R.
/ Ponath, Paul D.
/ Post, Theodore W.
/ Qin, Shixin
/ TITLE OF INVENTION: G PROTEIN-COUPLED RECEPTOR GENE CCR3 AND
/ ANTAGONISTS THEREOF
/ NUMBER OF SEQUENCES: 18
/ CORRESPONDENCE ADDRESS:
/ ADDRESS: Hamilton, Brook, Smith & Reynolds, P.C.
/ STREET: Two Militia Drive
/ CITY: Lexington
/ STATE: MA
/ COUNTRY: USA
/ ZIP: 02173
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/283,028
/ FILING DATE: 28-Oct-2002
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; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/720,565
; FILING DATE: 30-SEP-1996
; APPLICATION NUMBER: PCT/US96/00608
; FILING DATE: 19-JAN-1996
; APPLICATION NUMBER: US 08/375,199
; FILING DATE: 19-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: LKS94-05A2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1689 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-283-028-1

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Query Match	84.9%	Score 380.4;	DB 6;	Length 1689;
Best Local Similarity	98.4%;	Pred. No. 3.4e-83;		
Matches 436;	Conservative	0;	Mismatches 2;	Indels 5;
				Gaps 5;

QY	7	AGATGCAGAAAATTGCTTAAAGAGAAAGGACCAAGGAGATGAAGCAACACATTAAAGCCT	66
Db	1251	AGATGCAGAAAATTGCTTAAAGAGAAAGGACCAAGGAGATGAAGCAACACATTAAAGCCT	1310
QY	67	TCCACACTCACCTCTTAAACAGTCCTTCAA-CTTCCAGTGCACACTGAAGCTCTTGA	125
Db	1311	TCCACACTCACCTCTTAAACAGTCCTTCAA-CTTCCAGTGCACACTGAAGCTCTT-AA	1369
QY	126	GACACTGAATATACACACAGCAGTAGCAGTAGATGCATGTACCCTAAGTCATTACCAC	185
Db	1370	GACACTGAATATACACACAGCAGTAGCAGTAGATGCATGTACCCTAAGTCATTACCAC	1429
QY	186	AGGCCAGGGGCTGGCAGCGTACTCATCAACCCTAAAGCAGAGCTTGTCTTCTCT	245
Db	1430	AGGCCA-GGGCTGGGACGCGTACTCATCAAC-CTAAAGCAGAGCTTGTCTTCTCT	1487
QY	246	CTCTAAATGAGTTACCTACATTTTAAATGCACCTGAATGTTAGATAGTTACTATATGCCG	305
Db	1488	CTCTAAATGAGTTACCTATATTTTAAATGCACCTGAATGTTAGATAGTTACTATATGCCG	1547
QY	306	CTACAAAAAGGTAAAACTTTTATATTTTATACATTAACTTCAGCCAGCTATTGTATATA	365
Db	1548	CTACAAAAAGGTAAAACTTTTATATTTTATACATTAACTTCAGCCAGCTATT-ATATTA	1606
QY	366	ATAAAACATTTTACACACAATACATAAGTTAACTATTTTATTTCTAATGTGCTAGTTC	425
Db	1607	ATAAAACATTTTACACACAATACATAAGTTAACTATTTTATTTCTAATGTGCTAGTTC	1666
QY	426	TTTCCCTGCTTAATGAAAAGCTT 448	
Db	1667	TTTCCCTGCTTAATGAAAAGCTT 1689	

RESULT 12
US-10-311-455-310/c
; Sequence 310, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Detect
; TITLE OF INVENTION: cytosine methylation
; FILE REFERENCE: 5013.1014

```

: CURRENT APPLICATION NUMBER: US/10/311,455
: CURRENT FILING DATE: 2002-12-16
: PRIOR APPLICATION NUMBER: PCT/EP01/07537
: PRIOR FILING DATE: 2001-07-02
: PRIOR APPLICATION NUMBER: DE 10032529.7
: PRIOR FILING DATE: 2000-06-30
: PRIOR APPLICATION NUMBER: DE 10043826.1
: PRIOR FILING DATE: 2000-09-01
: NUMBER OF SEQ ID NOS: 2424
: SEQ ID NO 310
: LENGTH: 7201
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-310

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Query Match	75.7%;	Score 33912;	DB 6;	Length 7201;
Best Local Similarity	84.8%;	Pred. No. 8.8e-73;		
Matches 380; Conservative	0;	Mismatches 68;	Indels 0;	Gaps 0;

[illegible]

RESULT 13
US-10-311-455-309
; Sequence 309, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determining Cytosine Methylation
; TITLE OF INVENTION: Cytosine methylation
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311,455
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01

; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 309
; LENGTH: 7201
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-309

Query Match 65.7%; Score 294.4; DB 6; Length 7201;
Best Local Similarity 78.6%; Pred. No. 9.4e-62;
Matches 352; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

QY 1 TAGGTCAGATGCAGAAATTCGCTTAAGAGGAGGACCAAGGATGAGCAACACAT 60
Db 6097 TAGGTTAGATGTAGAAATTCGTTAAAGAGGAGGATTAAGGAGATGAAATATAT 6156
QY 61 AAGCCTTCACACTCACCCTCTAAGACAGTCCTCAAACTTCCAGTGAACACTGAGCTC 120
Db 6157 AAGTTTTTATATTTATTTTAAATAGTTTTTTAAATTTTATGTTATATTAAGTTT 6216
QY 121 TTGAAGACACTGAATATATACACAGCAGTAGCAGTAGATGATGTAACCTAAGTCATT 180
Db 6217 TTGAAGATATGAAATATATATATAGTAGTAGTAGATGATGTAATTTAAGTTATT 6276
QY 181 ACCACAGGCCAGGGGCTGGCAGCGTACTCATCAACCCCTAAAGACAGAGCTTTGCT 240
Db 6277 ATTAATAGTTAGGGGTGGTAGCGTATTTATTTATTTAATAAGTAGAGTTTGT 6336
QY 241 TCTCTCTTAAATGAGTTACCTACATTTTAATGCACCTGAATGTTAGATAGTTACTATA 300
Db 6337 TTTTTTTAAATGAGTTATTTATTTAATGTATTTGAATGTTAGATAGTTATATA 6396
QY 301 TGCCGCTACAAAAAGGTAAACTTTTATATTTTATACATTAACTTCAGCCAGCTATTGA 360
Db 6397 TGTCGTTATAAAAAAGTAAATTTTATATTTTATATATTAATTTAGTTAGTTATGA 6456
QY 361 TATAAATAAAACATTTTCACACATACATAAGTTAACTATTTTCTAATGTGCT 420
Db 6457 TATAAATAAAATATTTTATATATATTAATTAAGTTAATTTTATTTTAAATGTGTT 6516
QY 421 AGTCTTCCCTGCTTAATGAAAAGCTT 448
Db 6517 AGTTTTTTTTTTGTTTATGAAAAGTTT 6544

RESULT 14
US-11-060-756-2216
; Sequence 2216, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; NUMBER OF SEQ ID NOS: 2005-02-18
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2216
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-060-756-2216

Query Match 23.4%; Score 105; DB 10; Length 600;
Best Local Similarity 100.0%; Pred. No. 1.4e-15;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAGGTCAGATGCAGAAATTCGCTTAAGAGGAGCAACGAGATGAAGCAACACATT 60
Db 496 TAGGTCAGATGCAGAAATTCGCTTAAGAGGAGCAACGAGATGAAGCAACACATT 555

QY 61 AAGCCTTCACACTCACCCTCTAATAACAGTCCTTCAAACTTCCAGT 105
Db 556 AAGCCTTCACACTCACCCTCTAATAACAGTCCTTCAAACTTCCAGT 600

RESULT 15
US-11-060-756-6488
; Sequence 6488, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; NUMBER OF SEQ ID NOS: 2005-02-18
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6488
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-060-756-6488

Query Match 23.4%; Score 105; DB 10; Length 600;
Best Local Similarity 100.0%; Pred. No. 1.4e-15;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAGGTCAGATGCAGAAATTCGCTTAAGAGGAGGAGCAACGAGATGAAGCAACACATT 60
Db 496 TAGGTCAGATGCAGAAATTCGCTTAAGAGGAGGAGCAACGAGATGAAGCAACACATT 555
QY 61 AAGCCTTCACACTCACCCTCTAATAACAGTCCTTCAAACTTCCAGT 105
Db 556 AAGCCTTCACACTCACCCTCTAATAACAGTCCTTCAAACTTCCAGT 600

Search completed: January 7, 2006, 20:31:33
Job time : 330.171 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 7, 2006, 05:45:42 ; Search time 1634.64 Seconds
(without alignments)
12822.754 Million cell updates/sec

Title: US-10-767-521-4

Perfect score: 448

Sequence: 1 taggtcagatgcagaaatt.....ccctgtcaatgaaagctt 448

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_hlc:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	387.4	86.5	747	2	BG220110 RST39882
2	159.6	35.6	640	7	CK953877 4093669 B
3	154.8	34.6	498	6	CB476821 jn812_E03
4	154.6	34.5	652	6	CF368588 853245 MA
5	154.6	34.5	683	7	CN153669 940808 MA
6	143.2	32.0	649	7	CK948708 4073860 B
7	134.6	30.0	475	11	CR922120 Sus scrofa
8	134.6	30.0	723	11	CR922142 Sus scrofa
9	105.6	23.6	1761	4	AK041106 Mus muscu
10	105.6	23.6	2396	4	AK089895 Mus muscu
11	93	20.8	2284	4	AK089875 Mus muscu
12	76.4	17.1	655	2	BB223728 BB223728
13	75	16.7	632	6	CF367184 841909 MA
14	71	15.8	657	7	CO683220 DG11-166f
15	67	15.0	832	7	CN155784 943112 MA
16	65.6	14.6	274	2	BF553209 UT-R-C2-n
17	49.4	11.0	320	2	BB225464 BB225464
18	49.4	11.0	1079	1	AJ927148 AJ927148
19	47.4	10.6	1203	10	CNS015WU
20	47.2	10.5	687	3	BP179101 BP179101
21	47.2	10.5	939	9	CC223760 CH261-48F
22	47.2	10.5	1027	10	CNS02750

23	47.2	10.5	1034	9	CC206179	CC206179 CH261-168
24	47.2	10.5	1086	9	CC258597	CC258597 CH261-93L
25	46.4	10.4	1101	10	CNS016LI	AL106896 Drosophila
26	46.2	10.3	421	10	CE644562	CE644562 t1gr-gss-
27	46.2	10.3	726	10	CZ668371	CZ668371 OM_Ba022
28	46.2	10.3	914	10	CNS00ZJY	AL097768 Drosophila
29	46	10.3	1101	10	CNS017ZQ	AL108704 Drosophila
30	45.8	10.2	975	10	CNS0102Y	AL098452 Drosophila
31	45.2	10.1	583	2	BG603853	BG603853 EST502943
32	44.6	10.0	874	9	AZ541515	AZ541515 ENTFQ60TF
33	44.6	10.0	1027	10	CNS02T50	AL212733 Tetraodon
34	44.4	9.9	1205	10	CNS0165A	AL106312 Drosophila
35	44.4	9.9	1341	10	AG430330	AG430330 Mus muscu
36	44.2	9.9	681	3	BP178582	BP178582 BP178582
37	44.2	9.9	829	9	BH501921	BH501921 BOHJ148TR
38	44.2	9.9	987	10	CNS014PQ	AL104456 Drosophila
39	44.2	9.9	1101	10	CNS0106X	AL098595 Drosophila
40	44	9.8	938	6	CD050219	CD050219 AGENCOURT
41	43.6	9.7	342	3	BP733312	BP733312 BP733312
42	43.6	9.7	538	1	AJ625164	AJ625164 AJ625164
43	43.6	9.7	699	9	AQ323327	AQ323327 RPT11-10
44	43.6	9.7	771	10	AG539796	AG539796 Mus muscu
45	43.6	9.7	1052	10	AG520832	AG520832 Mus muscu

ALIGNMENTS

RESULT 1	BG220110/c	747 bp	mRNA	linear	EST 21-APR-2001
LOCUS	RST39882	Athersys RAGE Library	Homo sapiens	CDNA	mRNA sequence.
DEFINITION	BG220110				
ACCESSION	BG220110				
VERSION	BG220110.1	GI:13746131			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 747)				
AUTHORS	Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J., Lerner,L., Costanzo,D., McKilligott,K., Boozar,S., Mays,R., Smith,B., Veloso,N., Kijka,A., Hess,J., Cothren,K., Lo,K., Offenbacher,J., Danzig,J. and Ducar,M. Creation of genome-wide protein expression libraries using random activation of gene expression Nat. Biotechnol. 19 (5), 440-445 (2001)				
TITLE					
JOURNAL					
PUBMED					
COMMENT	Contact: Scott J. Cain Athersys, Inc. 3201 Carnegie Ave, Cleveland, OH 44115, USA Tel: 216 431 9900 Fax: 216 361 9596 Email: scain@athersys.com High quality sequence stop: 523. location/Qualifiers 1..747 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /cell_line="HT1080" /clone_lib="Athersys RAGE Library" /note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."				
FEATURES	source				
ORIGIN					
Query Match	86.5%	Score 387.4;	DB 2;	Length 747;	

	Best Local Matches	Similarity	98.5%; Conservative	Pred. No. 4.5e-84; 0; Mismatches	Indels	Gaps
QY	1	TAGGTCA	GATGCAGAAAATGCTTAAAGAGGAGCAAGGATGAAGCAACACATT	60		
Db	403	TAGGTCA	GATGCAGAAAATGCTTAAAGAGGAGCAAGGATGAAGCAACACATT	344		
QY	61	AAGCCTT	CCACACTCACCTCTTAAACAGTCCCTTCAAACCTCCAGTGCACACACTGAAAGCTC	120		
Db	343	AAGCCTT	CCACACTCACCTCTTAAACAGTCCCTTCAAACCTCCAGTGCACACACTGAAAGCTC	284		
QY	121	TTGAAGAC	ACTGAAATATACACACAGCAGTAGCAGTAGATGCACTGTAACCTTAAGGTCATT	180		
Db	283	TTGAAGAC	ACTGAAATATACACACAGCAGTAGCAGTAGATGCACTGTAACCTTAAGGTCATT	224		
QY	181	ACCACAGG	CCAGGGGCTGGGCGACGCTCATCATCAACCCCTAAAGCAAGAGCTTTGCT	240		
Db	223	ACCACAGG	CCAGGGGCTGGGCGACGCTCATCATCAACCCCTAAAGCAAGAGCTTTGCT	164		
QY	241	TCTCTCT	TAAATGAGTTACTTACATTTTAAATGCACCTGAATGTTAGATAGTTACTATA	300		
Db	163	TCTCTCT	TAAATGAGTTACTTACATTTTAAATGCACCTGAATGTTAGATAGTTACTATA	104		
QY	301	TGCCGCTA	CAAAAAGGTAAACCTTTTATATTTTATACATTAACTTCAGCCAGCTAATTGA	360		
Db	103	TGCCGCTA	CAAAAAGGTAAACCTTTTATATTTTATACATTAACTTCAGCCAGCTAATTGA	44		
QY	361	TATTAAT	TAAACATTTTCAACAATAACAATAAGTTAA	397		
Db	43	TATTAAT	TAAACATTTTCAACAATAACAATAAGTTAA	7		

```

RESULT 2
LOCUS      CK953877/c
DEFINITION 4093669 BARC 10BOV Bos taurus cDNA clone 10BOV32_h12 3', mRNA
ACCESSION  CK953877
VERSION     CK953877
KEYWORDS    CK953877.1  GI:45468257
SOURCE      EST.
ORGANISM    Bos taurus (cow)
            Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1 (bases 1 to 640)
AUTHORS     Sonstegard, T.S., Van Tassel, C.P., Matukumalli, L.K., Harhay,
            G.P., Bosak, S., Rubenfield, M. and Gasbarre, L.C.
            Production of EST from cDNA libraries derived from immunologically
            activated bovine gut
TITLE       Unpublished (2004)
JOURNAL     Contact: Tad S. Sonstegard
COMMENT     Bovine Functional Genomics Laboratory
            Animal and Natural Resources Institute
            Bldg. 200 Rm2A BARC-East, Beltsville, MD 20705, USA
            Tel: 3015048416
            Fax: 3015048414
            Email: tads@anri.barc.umd.edu
            Single pass sequencing. Bases called and trimmed with phred
            0.000925 using options -trim_alt "-trim_fasta. Vector identified
            by cross_match using options -mismatch 12 -minscore 18
            Plate: 32 row: H column: 12
            Seq primer: AGCGATACCAATTCCACACAGG
            High quality sequence stop: 640.
FEATURES
Source      1..640
Location/Qualifiers

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FEATURES	Location/Qualifiers
Source	1..640
	/organism="Bos taurus"
	/mol_type="mRNA"
	/strain="Holstein"
	/db_xref="taxon:9913"
	/clone="10BOV32_H12"
	/sex="Male"
	/tissue_type="Pooled"

```

/dev_stage="Multiple"
/lab_host="DH10B T1 phage resistant"
/clone_lib="BARC 10BOV"
/note="Organ: Small Intestine; Vector: pagen-1; Site_1:
ECORV; Site_2: NotI; Equimolar amounts of mRNA extracted
from proximal jejunum of 18 and 21 wk old steers, and
distal ileums of 14 day old calves. proximal jejunum
exposed to C. oncophora for 3 and 6 weeks, and distal
ileum exposed to C. parvum for 7 days"

```

Query Match	35.6%;	Score 159.6;	DB 7;	Length 640;
Best Local Similarity	73.4%;	Pred. No. 2.6e-28;		
Matches 279;	Conservative	0;	Mismatches 79;	Indels 22;
				Gaps 5;
QY	1	TAGGTGAGATGCAGAAAATTGGCCTTAAAGAGGAAGGACCAAGGAGATGAAAGCAACACAT	60	
DB	375	TAGGTGAGATGCAGAACATTGGCCTTAAAGAGATGTACAGAACAGATGAAGCCACACATC	316	
QY	61	AAGCCTTCCACACTGACCTCTAAAACAGTCTTCAAACCTTCCAGTGCAACACTGA-AGCT	119	
DB	315	G-----ACCTCTTCCACCAAGTCTTTGGACTTCCAGCACAATGGCCATAGCT	270	
QY	120	CTTGAAGACACTGAATATATACACACAGCAGTAGCAGTAGCATGTACCTTAAGGTCAT	179	
DB	269	CTTGAAGCCATTAAATATATATACACAAATGGTGAAGGTATCTATGCAACCCCAAGTCAT	210	
QY	180	TACCACAGGCCAGGGCGTGGGACGCGTACTCATCATCAACCCCTAAAAGCAGAGCTTTGC	239	
DB	209	TACCAAGGTCACGGCTGGACAATG-ACCTTTTATGAACCTGAAAAGCAGAGCTTTGC	151	
QY	240	TTCTCTCTTAAATGAGTTACCTACATTTTAAATGACCTGAATGTTAGATGTTACTAT	299	
DB	150	TTGATTCACTCGAGTCACATA-----ATTTAAATGCACTGAATGTTAGATGTTACTAT	96	
QY	300	ATGCCGCTACAAAAGGTAAAACTTTTATATTTTATACATTAACCTTCAGCCAGCTATTG	359	
DB	95	ATGCAGCTATACTA-CTCAAGCTTTTATATCTTAAATCTTAACCTTCAGCCAGTATTG	37	
QY	360	ATATTAATTAACATTTTCA	379	
DB	36	ATATTAATGAACATATATA	17	

RESULT 3
 CB476821/c
 LOCUS 498 bp mRNA linear EST 26-MAR-2003
 DEFINITION jns12.B03.f jns Sus scrofa cDNA \$', mRNA sequence.
 ACCESSION CB476821
 VERSION CB476821.1 GI:29283207
 KEYWORDS EST.
 SOURCE Sus scrofa (pig)
 ORGANISM Sus scrofa
 BUKARYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 MAMMALIA; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
 Sus.
 REFERENCE 1 (bases 1 to 498)
 AUTHORS Neilan,J.G., Kutish,G.F., Lu,Z., Zsak,A. and Rock,D.L.
 TITLE Sequence analysis of African swine fever virus infected and
 non-infected porcine macrophage cDNA libraries
 JOURNAL unpublished (2003)
 COMMENT Contact: Neilan JG

FEATURES

Email: jneilan@piadc.ars.usda.gov

Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim alt option. Vector identified by cross_match v0.990329 and lucy v1.17p.

Seq primer: M13 Forward.

Location/Qualifiers

FEATURES

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1. .498
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/tissue_type="lymphoid"
/cell_type="macrophage"
/lab_host="DH10B"
/clone_lhb="jns"
/notes="Vector: pSPORT1; Site 1: NotI; Site 2: SalI;
Library made from pools of polyA selected RNA. Macrophages
were derived from peripheral blood mononuclear cells
cultured for 48 hrs on plastic in the presence of 30% L929
supernatant."

```

ORIGIN

Query Match	34.6%;	Score 154.8;	DB 6;	Length 498;
Best Local Similarity	73.6%;	Pred. No. 3.7e-27;		
Matches 281; Conservative	0;	Mismatches 87;	Indels 14;	Gaps 6;

QY	29	AGGAAGGACCAAGGAGATGAGCAACAACATTAAGCCTTCCACACTCACTCTTAACAAG	88
Db	370	AGGTCAGATGCAGAACATTGTTTGAAGAGAGTGAAGCAATATACATTGAACCTCTATACCAG	311
QY	89	TCCTTCAAACTTCCAGTGCACAACACTGAAAGCTCTTGAAGACACTGAAATATACACAGCA	148
Db	310	TCCTTTGAACCTTCCAGCACAGCACTGAAAGCT-TTGAAGACATTAATAATATATACCAATG	252
QY	149	GTAGCAGTAGATGCATGTACCCCTAAGGTCATTAACAAGGCCAGGGGCTGGGACGCTAC	208
Db	251	GTGAGGTATATCTATGCACCCCAAGTCATTAACCAAGSTCAATGTTGGCAGTG-AC	193
QY	209	TCATCATCAACCCCTAAAGCAGAGCTTGGCTCTCTCTTAAATGAATTACCTACATT	268
Db	192	TGCGTGTCAACCCCTGAAGACGAGAGCTTGGCTGATTCTCTCA--GAGTTACATACATT	135
QY	269	TTAATGCACCTGAATGTTAGATAGTTACTATATATGCCGCTACAAAAAGGTAAACCTTTTA	328
Db	134	TTAATGCACCTGAA-GTTAGATAGTTACTATATATGCAGCTACAAACAAGTAAGCTTATCT	76
QY	329	TATTTTATACATTAACTTCAGCCCAAGCTATGATATAATTAACAAT-TTTCACACATAAC	387
Db	75	TCTTTT-----ACTTCAGCCAGTTATTGACATAAAGGAACATATTTTCACAAATAC	24
QY	388	AATAAGTTAACTATTTTATTTT	409
Db	23	AATTAATCGATTACATTCCTTT	2

[illegible]

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 652)	Smith, T.P.L., Freking, B.A., Ford, J.J., Vallet, J.L., Fox, J., Wise, T.A., Nonneman, D.J., Wray, J.B. and Keeler, J.W.	A second set of porcine ESTs from a pooled-tissue normalized library	Unpublished (2003)	Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and

```
trimmed with the aid of the trim_alt option. Vector identified with
cross_match v0.990329.
plate: SRG8025 row: 1 column: 17
Seq primer: TAGAAGGCACACTCGAGG.
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FEATURES

Source

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/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lhb="MARC 3Pig"
/note="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI;
library made with RNA pooled from multiple tissues
including brain, liver, muscle, placenta/endometrium,
ovary, testes, and bone marrow."
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ORIGIN

Query Match	34.5%;	Score 154.6;	DB 6;	Length 652;
Best Local Similarity	74.0%;	Pred. No. 4.3e-27;		
Matches 279;	Conservative 0;	Mismatches 84;	Indels 14;	Gaps 6;

QY	29	AGGAAGGACCAAGGAGATGAAGCAAAACA	CATTAAAGCTTCCACACTCACCTCTAAACAG	88	
Db	375	AGGTCAAGTGCAGAACATTGTCTGAAGAGATGAAGCAATA	CATTGAACCTCTATACCAG	316	
QY	89	TCCTTCAAACTTCCAGTGCACA	CTGAAGCTCTTGAAGACA	CTGAAATATACACAGCA	148
Db	315	TCCTTGAACCTTCCAGCACAGCACTGAAGCTC	-TGAAGACATTAAATATATATACACAATG	257	
QY	149	GTAGCAGTAGAGTCATGTACCCTTAAGGTCATTACCA	CAGGCCAGGGGCTGGGCAAGCTAC	208	
Db	256	GTGAGGTATATCTATGCACCCCAAAAGTCATTACCAAAAGTCA	TGTTGGGCAAGTGC	198	
QY	209	TCATCATCAACCTTAAAGACAGAGCTTTGCTTCTCTCTAAATGAGTTACCTACATT	268		
Db	197	TCGTGTCAACCTGGAAGACAGAGCTTTGCTTGA	TTCTCTCAA--GAGTTACATACATT	140	
QY	269	TTAATGCACCTGAATGTTAGATAGTTACTATATGCGGCTACAAAAGGTAAAACTTTTA	328		
Db	139	TTAATGCACCTGAA-GTTAGATAGTTACTATATGACGCTACAAACAAGTAAAGCTTATCT	81		
QY	329	TATTTTATACATTAACTTCAGCCAGCTATTGATATATAATATAAACAT	-TTTCAACAATAC	387	
Db	80	TCTTTT-----ACTTCAGCCAGTTATTTGACATRAAAGGAAACATATTTTCA	CAAAATAC	29	
QY	388	AATTAAGTTAACTAATTTT	404		
Db	28	AATTAATGCATTACATT	12		

RESULT 5					
CN153669/c					
LOCUS	CN153669	683 bp	mRNA	linear	EST 02-APR-2004
DEFINITION	940808 MARC 4P1G Sus scrofa cDNA 3', mRNA				
ACCESSION	CN153669				
VERSION	CN153669.1	GI:46168099			
KEYWORDS	EST.				
SOURCE	Sus scrofa	(pig)			
ORGANISM	Sus scrofa				

REFERENCE	1 (bases 1 to 683)
AUTHORS	Smith, T.P.L., Freking, B.A., Ford, J.J., Vallet, J.L., Wise, T.A., Nonneman, D.J., Wray, J.B. and Keèle, J.W.
TITLE	Porcine EST collection using a normalized library constructed from embryos representing early developmental stages
JOURNAL	unpublished (2003)
COMMENT	Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366

Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified with cross match v0.990329.
plate: TMM8048 row: L column: 9
Seq primer: TAGAAGCAGTCGAGG.
Location/Qualifiers
1..683

FEATURES
Source

/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 4P1G"
/note="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI;
library made with combined RNA from day-10, day-13,
day-15, day-25, and day-30 whole embryos."

ORIGIN

Query Match 34.5%; Score 154.6; DB 7; Length 683;
Best Local Similarity 74.0%; Pred. No. 4.3e-27;
Matches 279; Conservative 0; Mismatches 84; Indels 14; Gaps 6;

QY 29 AGGAAGACCAAGAGATGAAGCAACATTAAAGCCTTCCACACTCAGCTCTAAACAG 88
Db 375 AGGTGAGATGCAAGACATTGTCTGAAGAAGTGAAGCAATATGACCTCTATACCA 316
QY 89 TCCTCAAACTTCCAGTCAACACTGAAGCTCTTGAAGACACTGAATATACACACGA 148
Db 315 TCCTTTGAACCTCCAGCACAGCACTGAAGCTC-TGAAGACATTAAATATATACACAATG 257
QY 149 GTAGCACTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 208
Db 256 GTGAGAGTATATCTATGACACCCCAAGTCAATTCACCAAGGTCAATGTTGGCAGTG-AC 198
QY 209 TCATCATCAACCCCTAAAGCAGAGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 268
Db 197 TCGTGTCAACCCCTGAAGAGCAGAGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 140
QY 269 TTAATGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 328
Db 139 TTAATGCACTGAA-GTTAGATGATGATGATGATGATGATGATGATGATGATGATGATG 81
QY 329 TATTTATACATTAACTTCAAGCAGCTATGATGATGATGATGATGATGATGATGATGATG 387
Db 80 TCTTTT-----ACTTCAAGCAGCTATGATGATGATGATGATGATGATGATGATGATG 29
QY 388 AATAAGTTAACTATTTT 404
Db 28 AATAATCGATTATATT 12

RESULT 6
CK948708/c 649 bp mRNA -linear EST 15-MAR-2004
LOCUS 4073860 BARC 10BOV Bos taurus cDNA clone 10BOV25_005 3', mRNA
DEFINITION
SEQUENCE
CK948708
CK948708.1 GI:45463088

ACCESSION
KEYWORDS
SOURCE
ORGANISM
Bos taurus (cow)
Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Sonstegard, T.S., Van Tassel, C.P., Matukumalli, L.K., Harhay, G.P., Bosak, S., Rubenfield, M. and Gasbarre, L.C.
Production of EST from cDNA libraries derived from immunologically activated bovine gut
Unpublished (2004)
Contact: Tad S. Sonstegard

Bovine Functional Genomics Laboratory
Animal and Natural Resources Institute
Bldg. 200 Rm2A BARC-East, Beltsville, MD 20705, USA
Tel: 3015048416
Fax: 3015048414
Email: tads@anri.barc.usda.gov
Single pass sequencing. Bases called and trimmed with phred 0.000925 using options -trim_alt "-trim fasta. Vector identified by cross match using options -mismatch 12 -minscore 18
plate: 25 row: O column: 05
Seq primer: AGCGATACCAATTTCACACAGG
High quality sequence stop: 649.
Location/Qualifiers
1..649

FEATURES
Source

/organism="Bos taurus"
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/strain="Holstein"
/db_xref="taxon:9913"
/clone="10BOV25_005"
/sex="Male"
/tissue_type="Pooled"
/dev_stage="Multiple"
/lab_host="DH10B T1 phage resistant"
/clone_lib="BARC 10BOV"
/note="Organ: Small Intestine; Vector: pagen-1; Site 1:
EcoRV; Site 2: NotI; Equimolar amounts of mRNA extracted from proximal jejunums of 18 and 21 wk old steers, and distal ileums of 14 day old calves, proximal jejunum exposed to C. oncophora for 3 and 6 weeks, and distal ileum exposed to C. parvum for 7 days"

ORIGIN

Query Match 32.0%; Score 143.2; DB 7; Length 649;
Best Local Similarity 72.6%; Pred. No. 2.7e-24;
Matches 276; Conservative 0; Mismatches 78; Indels 26; Gaps 6;

QY 1 TAGGTCAAGTGCAGAAATGCTTAAAGCAAGACCAAGAGATGAAGCAACACTT 60
Db 371 TAGGTCAAGTGCAGAAATGCTTAAAGCAAGATGTACAGACAGTGAAGCCACACTC 312
QY 61 AAGCTTCCACACTCAGCTCTTAAACAGTCTTCAAACTTCCAGTGCACACTGA-AGCT 119
Db 311 G-----ACCTCTTCAACAGTCTTGGACTTCCAGCACAAATGGCCATAGCT 266
QY 120 CTGGAAGACACTGAATATACACAGCAGTAGCAGATGATGATGATGATGATGATGATG 179
Db 265 CTGGAAGCATTAAATATATACAAATGCT---GACGGTATTTATGCCAAAGTCAAT 210
QY 180 TACCAAGGCCAGGGGCTGGCAGCGTACTCATCATCAACCTAAAGCAGAGCTTGC 239
Db 209 TACCAAGGTCAACGCGTGCACAATG-ACCTTTATGAAACCTGAAAAAGCAGAGCTTGC 151
QY 240 TTCTCTCTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 299
Db 150 TTGATTCACTCGAGTCACTA-----ATTTAATGACCTGAATGTTAGATGTTACTAT 96
QY 300 ATGCCGCTACAAAAAGTTAACTTTTATATTTATATATTAATTCACTTCAAGCAGCTATTG 359
Db 95 ATGCAAGCTTAATACTA-GTCAAGCTTTTATATCTTAATCTTAATCTTCAAGCAGCTATTG 37
QY 360 AATATAATTAACATTTTCA 379
Db 36 AATATAATGAACATTAATAA 17

RESULT 7
CR922120/c 475 bp DNA -linear GSS 24-NOV-2004
LOCUS CR922120
DEFINITION Sus scrofa BES, genomic survey sequence.
ACCESSION CR922120
VERSION CR922120.1 GI:56262857
KEYWORDS GSS; Bac-end sequence BES; Genome Survey Sequence.
SOURCE Sus scrofa (pig)

	PUBMED	10349636	
REFERENCE	AUTHORS	Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.	
TITLE		Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes	
JOURNAL		Genome Res. 10 (10), 1617-1630 (2000)	
PUBMED		11042159	
REFERENCE	AUTHORS	Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watabiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.	
TITLE		RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer	
JOURNAL		Genome Res. 10 (11), 1757-1771 (2000)	
PUBMED		11076861	
REFERENCE	AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.	
TITLE		Functional annotation of a full-length mouse cDNA collection	
JOURNAL		Nature 409, 685-690 (2001)	
REFERENCE	AUTHORS		
TITLE		The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.	
JOURNAL		Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs	
REFERENCE	AUTHORS	Nature 420, 563-573 (2002)	
TITLE		6 (bases 1 to 1761)	
JOURNAL		Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiroake,T., Hirozane,T., Horii,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Koijima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.	
TITLE		Direct Submission	
JOURNAL		Submitted (16-JUL-2001) Yoshinide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)	
COMMENT		cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.	
FEATURES		Please visit our web site for further details.	
SOURCE		URL:http://genome.gsc.riken.jp/ URL:http://fantom.gsc.riken.jp/. location/Qualifiers	
		1..1761	
		/organism="Mus musculus"	
		/mol_type="mRNA"	
		/strain="C57BL/6J"	
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		/db_xref="taxon:10090"	
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		/sex="male"	
		/tissue type="aorta and vein"	
		/clone_lib="RIKEN full-length enriched mouse cDNA library"	
		/dev_stage="adult"	
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/note="unnamed protein product; chemokine (C-C) receptor 3
(MGD|MGI:104616, GB|NM_009914, evidence: BLASTN, 99%,
match=1080)
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/codon_start=1
/protein_id="BAC30823.1"
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	Query Match	23.6%;	Score 105.6;	DB 4;	Length 1761;	
	Best Local Similarity	58.1%;	Pred. No. 4.8e-15;			
	Matches 257;	Conservative 0;	Mismatches 159;	Indels 26;	Gaps 3;	
OY	13 AGAAATTCCTTAAAGAGGAGACCAAGGAGTAGAAGCAAACAATTAAAGCCTTCCACA	72				
Db	1303 AGAAATTTGTACTTAATTCATGGAAGTGAAAGTGAAGCAAACAATTAAAGTCACTCAC	1362				
OY	73 CTCACCTTAAACAGATCCTTCAAACTTCCAGTCAACACTGAAGCTCTTGAAGCACTG	132				
Db	1363 ATGACCTTAGCTCAGTCACTTTGTACTCTCCATGCATGCTGATGCTCTCAAGAAGCTGT	1422				
OY	133 AAATATACACACAGCAGTAGCAGTAGATGCAATGACCCTAAGGTCATTACCAAGGCCAG	192				
Db	1423 AAACACACATAATATACAGCATATATCTTCACTTACCCCAAGATCATTAGTAGAGGACAT	1482				
OY	193 GGGCTGGCGACGCTACTCATCAACCT-----AAAAAGCAGAGCTTGCCTCTC	246				
Db	1483 GTGCTGGCCAGTTGACAAATTCATCAACATGACATGAAAAGACAGCTTTTTTTTTTAT	1542				
OY	247 TCTAAATGAGTTACCTACATTTTAATGCACTGGAATGTTAGATAGTTACTATATGCGGC	306				
Db	1543 TCTCCAAGAGTTATACATGTTCTGATTCACTTAAATGTTAAATAAT-----CC	1591				
OY	307 TACAAAAGGTAAACTTTTATATTTATTCATTAACCTCAGCCAGCTAATGATATATAA	366				
Db	1592 ATTCAACAAGTAGAAGGTTTAAAAATATTTAACTACTTTTGCCACTTTTGACATCAG	1651				
OY	367 TAAACAATTTTCACACAATACAATAAGTTAACATTTTATTTTCTAATGTCCTAGTTCT	426				
Db	1652 TGAAATGTT-----TCACAAAATGCATTTATTTTATTTCTTAACGTAAGTAGTTCT	1702				
OY	427 TTCCCTGCTTAATGAAAAGCTT 448					
Db	1703 TTTCTTCTTGATGAATGGCTT 1724					
RESULT 10						
AK089895		2396 bp	mRNA	linear	HTC 03-APR-2004	
LOCUS	AK089895					
DEFINITION	Mus musculus activated spleen cDNA, RIKEN full-length enriched library, clone:F830047J12 product:chemokine (C-C) receptor 3, full insert sequence.					
ACCESSION	AK089895					
VERSION	AK089895.1 GI:26354724					
KEYWORDS	HTC; CAP trapper.					
SOURCE	Mus musculus (house mouse)					
ORGANISM	Mus musculus					
	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.					
REFERENCE	1 Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999) 10349636					
REFERENCE	2					

AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Komno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)
PUBMED	11042159
REFERENCE	3
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Komno, H., Akiyama, J., Nishi, K., Kitsuami, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)
PUBMED	11076861
REFERENCE	4
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE	Functional annotation of a full-length mouse cDNA collection
JOURNAL	Nature 409, 685-690 (2001)
PUBMED	11076861
REFERENCE	5
AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL	Nature 420, 563-573 (2002)
PUBMED	6 (bases 1 to 2396)
REFERENCE	6
AUTHORS	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuta, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Komno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
TITLE	Direct Submission
JOURNAL	Submitted (16-APR-2002)
PUBMED	Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
COMMENT	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge. Please visit our web site for further details. URL: http://genome.gsc.riken.jp/ URL: http://fantom.gsc.riken.jp/. Location/Qualifiers 1. 2396 /organism="Mus musculus" /mol_type="mRNA" /strain="NOD" /db_xref="FANTOM DB:F830047J12" /db_xref="taxon:10090" /clone="F830047J12" /tissue_type="activated spleen" /clone_lib="RIKEN full-length enriched mouse cDNA library" 86. 1165

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/note="unnamed protein:product; chemokine (C-C) receptor 3
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ITWGLAGLALPEFIPEHSQDSFGFSGSPRYPEGBEDSWKRFHALRNINIGALPLLI
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LPGBKMERBTSSVSPSTGQEIISVVP"

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ORIGIN			
Query Match	23.6%;	Score 105.6;	DB 4; Length 2396;
Best Local Similarity	58.1%;	Pred. No. 5e-15;	
Matches 257; Conservative	0;	Mismatches 159;	Indels 26; Gaps 3;

OY	13	AGAAATTTGCCTTAAGAAGGACCAAGAGATGAAGCAAACAATTAAAGCTTCCACA	72
Db	1174	AGAAATTTGTCACTTATTTCCATGGACTGAAGAGTAGAACAACATTAAAGTCAGTCACA	1233
OY	73	CTCACCCTTAAAACAGTCCCTTCAAACTTCCAGTGCAACACTGAAGCTCTTGAAGCACTG	132
Db	1234	ATGACCTCTAGCTCAGTCATTGTGTACTCTCCATGCCAATGCTGATGCTCTCAAGAAGCTGT	1293
OY	133	AAATATACACACAGCAGTAGCAGTAGATGCACTGTACCCTTAAGGTCATTACCAAGGCCAG	192
Db	1294	AAACACACATAATTAAC TGACAGATATCTTCATCTAACCCCAAGATCATTAAGTAGAGACAT	1353
OY	193	GCGTGGGCAAGCTACTCATCATCAACCT-----AAAAGCAGAGCTTGTCTCTC	246
Db	1354	GTGCTGGCCAGTGCACAATTCATCAAAACATGACATGAAGAAAAAGACAGCTTTTTTTTAT	1413
OY	247	TCTAAATGAGTTACCTACATTTTAATGACCTGAATGTTAGATAGTTACTATATGCGCG	306
Db	1414	TCTCCAAAAGATTATACATGTTCTGATTCACTTAAATGTTAAATAAT-----CC	1462
OY	307	TACAAAAAGTTAAAACTTTTATATTTTATACATTAACCTTCAGCCAGCTATGATATAAA	366
Db	1463	ATTCCACAAGTAGGAAGGTTTAAAAAATATTTAAACTACTTTTGCCACTTTTGACATCAG	1522
OY	367	TAAACACTTTTCACACAATACAAATAGTTAACTATTTTATTTCTAATGTCCTAGTTCT	426
Db	1523	TGAATATGTT-----TCACAAAATGCATTATTTTATTTCTTAACGTAAGTAGTTCT	1573
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LOCUS	DEFINITION	AK089875	2284 bp	mus musculus activated spleen cDNA, RIKEN full-length enriched library, clone: F830035018	product: chemokine (C-C) receptor 3, full insert sequence.	AK089875	2284 bp	mus musculus activated spleen cDNA, RIKEN full-length enriched library, clone: F830035018	product: chemokine (C-C) receptor 3, full insert sequence.
LOCUS	DEFINITION	AK089875	2284 bp	mus musculus activated spleen cDNA, RIKEN full-length enriched library, clone: F830035018	product: chemokine (C-C) receptor 3, full insert sequence.	AK089875	2284 bp	mus musculus activated spleen cDNA, RIKEN full-length enriched library, clone: F830035018	product: chemokine (C-C) receptor 3, full insert sequence.

ACCESSION	AK089875
VERSION	AK089875.1
KEYWORDS	HTC; CAP trapper.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus

Eukaryota; Metazoa; Chordata; Ctenata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1
AUTHORS Carninci, P. and Hayashizaki, Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
PUBMED 10349636
REFERENCE 2

AUTHORS	Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL PUBMED	Genome Res. 10 (10), 1617-1630 (2000)
REFERENCE	11042159
AUTHORS	3 Shibata,K., Itch,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsuai,T., Tashiro,H., Itch,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kasaiwagi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watabiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kita,A. and Hayashizaki,Y.
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL PUBMED	Genome Res. 10 (11), 1757-1771 (2000)
REFERENCE	11076861
AUTHORS	4 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE	Functional annotation of a full-length mouse cDNA collection
JOURNAL PUBMED	Nature 409, 685-690 (2001)
REFERENCE	5
AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL PUBMED	Nature 420, 563-573 (2002)
REFERENCE	6 (bases 1 to 2284)
AUTHORS	Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoaka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itch,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
TITLE	Direct Submission
JOURNAL	Submitted (16-APR-2002)
COMMENT	Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge. Please visit our web site for further details. URL:http://genome.gsc.riken.jp/ URL:http://fantom.gsc.riken.jp/. Location/Qualifiers 1. .2284 /organism="Mus musculus" /mol_type="mRNA" /strain="NOD" /db_xref="PANTOM DB:F830035O18" /db_xref="taxon:I0090" /clone="F830035O18" /tissue_type="activated spleen" /clone_lib="RIKEN full-length enriched mouse cDNA library" 215. .1294

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Oy	73 CTCACCTCTAAAAACAGTCCTTCAAACTTC-CAGTGCAACACTGAAGCTCTGAAGAACT 131
Db	1363 ATGACCTTAGGTCAAGTCATTGTAGGCTTCATGCCATGCTGATGCTCTCGAAGAACTG 1422
Oy	132 GAAATATACACACAGCAGTAGCAGTAGATGATGATCACTTAAGGTCAATTAACAGGCCA 191
Db	1423 TAAACACACATATACTACGACAGATATGTTCAATGTAACCAAGATCATTAAGTAGAGACA 1482
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Db	1483 TGTGCTGGCCAGTTGACAAATTCATCAAAACATGACATGAAGAAAAGACAGCTTTTGTGTA 1542
Oy	246 CTCTAAATGAGTTAATCTACATTTTAATGCACTGAATGTTAGATAGTTACTATATGCCG 305
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Oy	306 CTACAAAAAGGTAAAACTTTTATATTATTATACATTAATCTCAGCCAGCTATTGATATA 365
Db	1592 CATTACAGTAGAAGGTTTAAAAATATTAAACTACTTTTGCCACTTTTGACATCA 1651
Oy	366 ATAACAATTTTCACACATACATACATTAAGTTAACTATTATTTCTAATGTGCTAGTTC 425
Db	1652 GTGAATGTT-----TCACAAATGCATTTATTATTCTTAACGTAAGTAGTTC 1702
Oy	426 TTTCCCTGCTTAATGAAAAAGCTT 448
Db	1703 TTTTCTTCTTGATGAATGGCTT 1725
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BB223728	655 bp mRNA linear EST 31-AUG-2001
LOCUS	BB223728 RIKEN full-length enriched, adult male aorta and vein Mus
DEFINITION	musculus cDNA clone A530083H05 3', mRNA sequence.
ACCESSION	BB223728
VERSION	BB223728.2 GI:15410154
SOURCE	EST.
ORGANISM	Mus musculus (house mouse)
KEYWORDS	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus. 1 (bases 1 to 655) Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J.,

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including brain, liver, muscle, placenta/endometrium,
ovary, testes, and bone marrow."

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QY 190 CAGGGGCTGGGAGCGTACTCATCTCAACCCCTAA 224
Db 599 CAATGTTGGGCAGTG-ACTCGTGTCAACCCCTGA 632

RESULT 14
LOCUS CO683220/c 657 bp mRNA linear EST 26-JUL-2004

DEFINITION DG11-166f13 DG11-kidney Canis familiaris cDNA 3', mRNA sequence.

ACCESSION CO683220

VERSION CO683220.1 GI:50631886

KEYWORDS EST.

SOURCE Canis familiaris (dog)

ORGANISM Canis familiaris

REFERENCE 1 (bases 1 to 657)

AUTHORS Schluteter,T., Hermann,J., Weindel,M., Schnette,D., Kranz,H.,

TITLE Dog arrayTAG cDNA clone collection

JOURNAL Unpublished (2004)

COMMENT Contact: Thomas Schluteter

CONTACT: Thomas Schluteter

Waldhoferstrasse 98, D-69123 Heidelberg, Germany

TEL: +49 6221 4038 150

FAX: +49 6221 4038 290

EMAIL: Thomas.Schluteter@lionbioscience.com.

LOCATION/Qualifiers

1..657

/organism="Canis familiaris"

/mol_type="mRNA"

/strain="Beagle"

/db_xref="taxon:9615"

/tissue_type="kidney"

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/lab_host="DH10B"

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/note="Organ: Kidney; Vector: Dog pBluescript LION"

ORIGIN

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QY 1 TAGGTGAGATGCAGAAATTGGCTTAAGAGGAGGAGCAAGAGATGAAGCAAAACATTT 60
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QY 61 AAGCTTCCACACTCCTTAAGAGAGTCTTCAAACTTCCAGTGCACCACTGAAGCTC 120

Db 94 AAGTTATCATGTGACCTCAACGCCAACCCCTTAAACTTCCAGCTCAATGCTGTAAACC 35
QY 121 TTGAAGACACTGAAATATATACACAGCAGTA 151
Db 34 TTAAGACATTTAAATATATATACACAATCGTA 4

RESULT 15
LOCUS CN155784 832 bp mRNA linear EST 02-APR-2004

DEFINITION 943112 MARC 4P1G Sus scrofa cDNA 5', mRNA sequence.

ACCESSION CN155784

VERSION CN155784.1 GI:46170214

KEYWORDS EST.

SOURCE Sus scrofa (pig)

ORGANISM Sus scrofa

REFERENCE 1 (bases 1 to 832)

AUTHORS Smith,T.P.L., Freking,B.A., Ford,J.J., Vallet,J.L., Wise,T.A.,

Noneman,D.J., Wray,J.E. and Keele,J.W.

Porcine EST collection using a normalized library constructed from

embryos representing early developmental stages

Unpublished (2003)

Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center

PO Box 166, Clay Center, NE 68933-0166, USA

TEL: 402 762 4366

FAX: 402 762 4390

Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called with phred v0.020425.c and

trimmed with the aid of the trim_alt option. Vector identified with

cross_match v0.990329.

Plate: TMM8048 row: L column: 9

Seq primer: GTAATACGACTCACTATAGGG.

LOCATION/Qualifiers

1..832

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/lab_host="DH10B"

/clone_lib="MARC 4P1G"

/note="Vector: pCDNA3.1; Site_1: EcoRI; Site_2: NotI;
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day-15, day-25, and day-30 whole embryos."

ORIGIN

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Best Local Similarity 67.9%; Pred. No. 1.2e-05;
Matches 108; Conservative 0; Mismatches 50; Indels 1; Gaps 1;

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Db 735 TCCTTGAACCTTCAGCAGCACTGAAGCTC-TGAAGACATTAATAATATATACAAATG 793
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Db 794 GTGAGGTATATCTATGCAACCCCAAGTCATTACCAAG 832

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Job time : 1637.64 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using SW model

Run on: January 7, 2006, 03:54:36 ; Search time 244.515 Seconds
(without alignments)
12211.020 Million cell updates/sec

Title: US-10-767-521-4

Perfect score: 448

Sequence: 1 taggtcagatgcagaaatt.....ccctgttaataaagctt 448

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_21:*

1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	448	100.0	1717	6	AAD25221 Human che
2	448	100.0	1717	6	AAD25245 Human che
3	448	100.0	1717	6	ABL67066 Thyroid c
4	448	100.0	1717	11	AD131633 Human CDN
5	448	100.0	1717	13	AD83700 Human lym
6	448	100.0	1915	2	AAT85162 Human che
7	448	100.0	1915	10	ADC03342 Human CDN
8	448	100.0	1915	13	ADT90848 Human che
9	448	100.0	1915	13	ADU47727 Human che
10	448	100.0	5099	2	AAT93601 Human eos
11	448	100.0	5791	8	ABZ68879 Nucleotid
12	448	100.0	5791	14	ADY86631 Human CC
13	380.4	84.9	1689	2	AAT31334 CC-chemok
14	380.4	84.9	1689	2	AAT58783 Human C-C
15	380.4	84.9	1689	2	AAV07402 Human C-C
16	380.4	84.9	1689	3	AAA35146 Human ade
17	380.4	84.9	1689	3	AAF21268 Human low
18	380.4	84.9	1689	6	ABL40462 Human C-C
19	380.4	84.9	1689	10	ABZ96962 Human nuc

20	380.4	84.9	1689	10	ABX13645	Abx13645 Human CDN
21	380.4	84.9	1689	11	ABD20811	ABD20811 Human pul
22	380.4	84.9	3958	3	AAA35147	Aaa35147 Human ade
23	380.4	84.9	3958	3	AAF21269	Aaf21269 Human low
24	380.4	84.9	3958	10	ABZ96963	Abz96963 Human nuc
25	380.4	84.9	3958	11	ABD20812	ABD20812 Human pul
26	339.2	75.7	7201	6	ABL32337	Ab132337 Human imm
27	294.4	65.7	7201	6	AB132336	Ab132336 Human imm
28	108	24.1	28140	12	AD047032	Ado47032 Human oli
29	108	24.1	42587	12	ADJ61642	Adj61642 Concateme
30	105	23.4	1201	3	AAA35145	Aaa35145 Human ade
31	105	23.4	1201	3	AAF21267	Aaf21267 Human low
32	105	23.4	1201	6	ABK84282	Abk84282 Human CDN
33	105	23.4	1201	8	ABZ42635	Abz42635 Human C-C
34	105	23.4	1201	10	ABZ96961	Abz96961 Human nuc
35	105	23.4	1201	10	ACA56487	Aca56487 Human sig
36	105	23.4	1201	11	ADI31579	Adi31579 Human CDN
37	105	23.4	1201	11	ABD20810	ABD20810 Human pul
38	105	23.4	1201	12	ADI56283	Adi56283 Human pol
39	105	23.4	1201	12	ADJ59499	Adj59499 CCR3 enco
40	105	23.4	1201	12	ADO44989	Ado44989 Human oli
41	105	23.4	1201	13	ADS83646	Ads83646 Human lym
42	105	23.4	1201	14	ADY15933	Ady15933 DNA encod
43	105	23.4	1201	14	ADY19619	Ady19619 DNA encod
44	50	11.2	50	6	ABZ02209	Abz02209 Human leu
45	46.8	10.4	7025	6	ABK40060	Abk40060 Human che

ALIGNMENTS

RESULT 1	
AAD25221	AAD25221 standard, DNA; 1717 BP.
ID	
XX	AAD25221;
AC	
XX	
DT	12-MAR-2002 (first entry)
XX	
DE	Human chemokine (C-C motif) receptor 3 (CCR3) gene #1.
XX	
KW	Human; chemokine (C-C motif) receptor 3; CCR3 gene; haplotyping;
KW	genotyping; type IV hypersensitivity reaction; HIV-1; gene therapy;
KW	human immunodeficiency virus 1; single nucleotide polymorphism; SNP;
KW	chromosome 3p21.3; ds.
XX	
OS	Homo sapiens.
XX	
FH	Key
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FT	location/Qualifiers
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FT	/standard name= "Single nucleotide polymorphism (SNP)"
FT	replace(197, A)
FT	/*tag= b
FT	/standard name= "Single nucleotide polymorphism (SNP)"
FT	205.1272
FT	/*tag= c
FT	/product= "Human CCR3 protein"
FT	/note= "This region corresponds to exon 1"
FT	replace(255, C)
FT	/*tag= d
FT	/standard name= "Single nucleotide polymorphism (SNP)"
FT	replace(1256, C)
FT	/*tag= e
FT	/standard name= "Single nucleotide polymorphism (SNP)"
XX	
PN	WO200187908-A2.
XX	
PD	22-NOV-2001.
XX	
PF	18-MAY-2001; 2001WO-US016278.
XX	
PR	18-MAY-2000; 2000US-0205191P.

(GENA-) GENAISSANCE PHARM INC.
 Choi JY, Kazemi A, Koshy B;
 WPI: 2002-055681/07.
 P-PSDB; AAE15320.

Isolated polymorphic variants of chemokine (C-C motif) receptor 3 (CCR3) gene useful for studying function of CCR3, expressing the CCR3 protein and to screen drugs to treat CCR3 activity-related diseases.

Example 1; Fig 1; 53pp; English.

The invention relates to genetic variants of human chemokine (C-C motif) receptor 3 (CCR3) gene. The invention also relates to compositions and methods for haplotyping and/or genotyping the CCR3 gene in an individual. Polynucleotides of the invention are useful for studying the expression and function of CCR3 and in expressing CCR3 proteins for use in screening candidate drugs to treat diseases related to CCR3 activity. They are also used in gene therapy. The polymorphism and haplotype data is useful for validating whether CCR3 is a suitable target for drugs to treat type IV hypersensitivity reactions and human immunodeficiency virus (HIV)-1, screening for such drugs and reducing bias cells in clinical trials of such drugs. The genotyping method is useful for determining whether an individual has one haplotype or haplotype pairs. The haplotyping method is useful for improving the efficiency and outcome of several steps in the discovery and development of drugs for treating diseases associated with CCR3 activity such as type IV hypersensitivity reactions and HIV-1. The present sequence is human CCR3 gene located on chromosome 3p21.3

Query Match	100.0%;	Score 448;	DB 6;	Length 1717;
Best Local Similarity	100.0%;	Pred. No. 1.4e-104;		
Matches 448;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY 1	TAGGTCAGATGCAGAAAATTGCGCTTAAGAGAGGAAGCAAGAGATGAAAGCAAAACACATT	60		
DB 1270	TAGGTCAGATGCAGAAAATTGCGCTTAAGAGAGGAAGCAAGAGATGAAAGCAAAACACATT	1329		
QY 61	AAGCCTTCACACACTCACCTCTAATAACAGTCCCTTCAAACTTCCAGTGCAACACTGAAAGCTC	120		
DB 1330	AAGCCTTCACACACTCACCTCTAATAACAGTCCCTTCAAACTTCCAGTGCAACACTGAAAGCTC	1389		
QY 121	TTGAAGACACTGMAATATATACACACAGCAGTAGCAGTAGCATGTACCCCTMAAGTCATT	180		
DB 1390	TTGAAGACACTGMAATATATACACACAGCAGTAGCAGTAGCATGTACCCCTMAAGTCATT	1449		
QY 181	ACCACAGGCGCAGGGGCTGGGCGACGTACTCATCATCAACCTTAAAAAGCAGAGCTTTGGCT	240		
DB 1450	ACCACAGGCGCAGGGGCTGGGCGACGTACTCATCATCAACCTTAAAAAGCAGAGCTTTGGCT	1509		
QY 241	TCTCTCTTAAATGAGTTTACTACATTTTAATGCACCTGAATGTTAGATAGTTACTATA	300		
DB 1510	TCTCTCTTAAATGAGTTTACTACATTTTAATGCACCTGAATGTTAGATAGTTACTATA	1569		
QY 301	TGCCGCTACAAAAAGGTAABACTTTTATATTTTATACATTAACTTCAGCCAGCTATTGA	360		
DB 1570	TGCCGCTACAAAAAGGTAABACTTTTATATTTTATACATTAACTTCAGCCAGCTATTGA	1629		
QY 361	TATTAATTAATAACATTTTTCACACATAACAATAAGTTAACTATTTTATTTTCTAATGTGCT	420		
DB 1630	TATTAATTAATAACATTTTTCACACATAACAATAAGTTAACTATTTTATTTTCTAATGTGCT	1689		
QY 421	AGTTCCTTCCCTGCTTAATGAAAAGCTT 448			
DB 1690	AGTTCCTTCCCTGCTTAATGAAAAGCTT 1717			

RESULT 2
AAD25245
ID AAD25245 standard; DNA; 1717 BP.

XX			
AC	AAD25245;		
XX			
DT	12-MAR-2002	(first entry)	
XX			
DB	Human chemokine (C-C motif) receptor 3 (CCR3) gene #2.		
XX			
KW	Human; chemokine (C-C motif) receptor 3; CCR3 gene; haplotyping;		
KW	genotyping; type IV hypersensitivity reaction; HIV-1; gene therapy;		
KW	human immunodeficiency virus 1; polymorphism; chromosome 3p21.3; ds.		
XX			
OS	Homo sapiens.		
XX			
FH			
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FT		/note= "This degenerate base represents polymorphic site	
FT		(PS) 1"	
FT		197	
FT	misc_feature	/*tag= b	
FT		/note= "This degenerate base represents polymorphic site	
FT		(PS) 2"	
FT		255	
FT	misc_feature	/*tag= c	
FT		/note= "This degenerate base represents polymorphic site	
FT		(PS) 3"	
FT		1256	
FT	misc_feature	/*tag= d	
FT		/note= "This degenerate base represents polymorphic site	
FT		(PS) 4"	

WO200187908-A2.

22-NOV-2001.

18-MAY-2001; 2001WO-US016278.

18-MAY-2000; 2000US-0205191P.

(GENA-) GENAISSANCE PHARM INC.

Choi JY, Kazemi A, Koshy B;

WPI; 2002-055681/07.

Isolated polymorphic variants of chemokine (C-C motif) receptor 3 (CCR3) gene useful for studying function of CCR3, expressing the CCR3 protein and to screen drugs to treat CCR3 activity-related diseases.

Claim 5; Page 53; 53pp; English.

The invention relates to genetic variants of human chemokine (C-C motif) receptor 3 (CCR3) gene. The invention also relates to compositions and methods for haplotyping and/or genotyping the CCR3 gene in an individual. Polynucleotides of the invention are useful for studying the expression and function of CCR3 and in expressing CCR3 proteins for use in screening candidate drugs to treat diseases related to CCR3 activity. They are also used in gene therapy. The polymorphism and haplotype data is useful for validating whether CCR3 is a suitable target for drugs to treat type IV hypersensitivity reactions and human immunodeficiency virus (HIV)-1, screening for such drugs and reducing bias cells in clinical trials of such drugs. The genotyping method is useful for determining whether an individual has one haplotype or haplotype pairs. The haplotyping method is useful for improving the efficiency and outcome of several steps in the discovery and development of drugs for treating diseases associated with CCR3 activity such as type IV hypersensitivity reactions and HIV-1. The present sequence is human CCR3 gene located on chromosome 3p21.3

Query Match	100.0%;	Score 448;	DB 6;	Length 1717;
Best Local Similarity	100.0%;	Pred. No. 1.4e-104;		
Matches 448;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 1 TAGGTGATGCGAAGAAATTCCTTAAAGAGGAGGACCAAGAGATGAGCAAAACATT 60
Db 1270 TAGGTGATGCGAAGAAATTCCTTAAAGAGGAGGACCAAGAGATGAGCAAAACATT 1329
QY 61 AAGCCTTCCACACTCACCCTCTTAAACAAGTCCCTTCAAACCTTCCAGTGCACACTGAAGCTC 120
Db 1330 AAGCCTTCCACACTCACCCTCTTAAACAAGTCCCTTCAAACCTTCCAGTGCACACTGAAGCTC 1389
QY 121 TTGAAGACACTGAATATATACACAGCAGTAGCAGTAGATGATGTACCCCTAAGGTCAAT 180
Db 1390 TTGAAGACACTGAATATATACACAGCAGTAGCAGTAGATGATGTACCCCTAAGGTCAAT 1449
QY 181 ACCACAGGCCAGGGGCTGGGCGAGCTACTCATCATCAACCCCTAAAGCAGAGCTTGGCT 240
Db 1450 ACCACAGGCCAGGGGCTGGGCGAGCTACTCATCATCAACCCCTAAAGCAGAGCTTGGCT 1509
QY 241 TCTCTCTTAAATGAGTTACCTACATTTTATGCACTGAATGTTAGATAGTACTATA 300
Db 1510 TCTCTCTTAAATGAGTTACCTACATTTTATGCACTGAATGTTAGATAGTACTATA 1569
QY 301 TGGCGCTACAAAAGGTAAACTTTTATATTTTATACATTAATTCAAGCCAGCTATTGA 360
Db 1570 TGGCGCTACAAAAGGTAAACTTTTATATTTTATACATTAATTCAAGCCAGCTATTGA 1629
QY 361 TATAATAATAAACATTTTCACACATACATAAGTTAACTATTATTCTTAATGTGCT 420
Db 1630 TATAATAATAAACATTTTCACACATACATAAGTTAACTATTATTCTTAATGTGCT 1689
QY 421 AGTTCTTCCCTGCTTAATGAAGCTT 448
Db 1690 AGTTCTTCCCTGCTTAATGAAGCTT 1717

RESULT 3
ABL67066
ID ABL67066 standard; DNA; 1717 BP.

XX ABL67066;
AC
XX
DT 15-MAY-2002 (first entry)
XX
DB Thyroid cancer related gene sequence SEQ ID NO:5403.
XX
KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KW gene; ds.
XX
OS Homo sapiens.
XX
PN WO200194629-A2.
XX
PD 13-DEC-2001.
XX
PF 30-MAY-2001; 2001WO-US010838.
XX
PR 05-JUN-2000; 2000US-0209473P.
PR 05-JUN-2000; 2000US-0209531P.
PR 18-SEP-2000; 2000US-0233133P.
PR 18-SEP-2000; 2000US-0233617P.
PR 20-SEP-2000; 2000US-0234009P.
PR 20-SEP-2000; 2000US-0234034P.
PR 20-SEP-2000; 2000US-0234052P.
PR 22-SEP-2000; 2000US-0234509P.
PR 22-SEP-2000; 2000US-0234567P.
PR 25-SEP-2000; 2000US-0234923P.
PR 25-SEP-2000; 2000US-0234924P.
PR 25-SEP-2000; 2000US-0235077P.
PR 25-SEP-2000; 2000US-0235082P.
PR 25-SEP-2000; 2000US-0235134P.
PR 25-SEP-2000; 2000US-0235280P.
PR 26-SEP-2000; 2000US-0235637P.

PR 26-SEP-2000; 2000US-0235638P.
PR 27-SEP-2000; 2000US-0235711P.
PR 27-SEP-2000; 2000US-0235720P.
PR 27-SEP-2000; 2000US-0235840P.
PR 27-SEP-2000; 2000US-0235863P.
PR 28-SEP-2000; 2000US-0236028P.
PR 28-SEP-2000; 2000US-0236032P.
PR 28-SEP-2000; 2000US-0236033P.
PR 28-SEP-2000; 2000US-0236034P.
PR 28-SEP-2000; 2000US-0236109P.
PR 28-SEP-2000; 2000US-0236111P.
PR 29-SEP-2000; 2000US-0236842P.
PR 29-SEP-2000; 2000US-0236891P.
PR 02-OCT-2000; 2000US-0237172P.
PR 02-OCT-2000; 2000US-0237173P.
PR 02-OCT-2000; 2000US-0237278P.
PR 02-OCT-2000; 2000US-0237294P.
PR 02-OCT-2000; 2000US-0237295P.
PR 02-OCT-2000; 2000US-0237316P.
PR 03-OCT-2000; 2000US-0237425P.
PR 03-OCT-2000; 2000US-0237598P.
PR 03-OCT-2000; 2000US-0237604P.
PR 03-OCT-2000; 2000US-0237606P.
PR 03-OCT-2000; 2000US-0237608P.
PR 01-NOV-2000; 2000US-0244867P.
PR 01-NOV-2000; 2000US-0245084P.
XX
XX
PA (AVAL-) AVALON PHARM.
XX
PI Young PR, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI Soppet DR, Weaver Z;
XX
XX WPI; 2002-188264/24.
XX
XX
PT Screening for anti-neoplastic agent involves exposing cells to a chemical
PT agent to be tested for anti-neoplastic activity, and determining a change
PT in expression of a gene of a signature gene set.
XX
XX
PS Claim 1; SEQ ID NO 5403; 44pp; English.
XX
XX
CC The present invention describes a method (M1) for screening for an anti-
CC neoplastic agent. The method involves exposing cells to a chemical agent
CC to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (I) of a signature gene set, where (I)
CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC to ABL70110), or is at least 95% identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening an
CC anti-neoplastic agent, and can be used for producing a product which is
CC the data collected with respect to the anti-neoplastic agent as a result
CC of M1, and the data is sufficient to convey the chemical structure and/or
CC properties of the agent. M1 can be used in the treatment of cancer such
CC as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
CC cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
CC tumour
XX
XX
SQ Sequence 1717 BP; 434 A; 428 C; 351 G; 504 T; 0 U; 0 Other;

Query Match 100.0%; Score 448; DB 6; Length 1717;
Best Local Similarity 100.0%; Pred. No; 1.4e-104;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TAGGTGATGCGAAGAAATTCCTTAAAGAGGAGGACCAAGAGATGAGCAAAACATT 60
Db 1270 TAGGTGATGCGAAGAAATTCCTTAAAGAGGAGGACCAAGAGATGAGCAAAACATT 1329
QY 61 AAGCCTTCCACACTCACCCTCTTAAACAAGTCCCTTCAAACCTTCCAGTGCACACTGAAGCTC 120
Db 1330 AAGCCTTCCACACTCACCCTCTTAAACAAGTCCCTTCAAACCTTCCAGTGCACACTGAAGCTC 1389
QY 121 TTGAAGACACTGAATATATACACAGCAGTAGCAGTAGATGATGTACCCCTAAGGTCAAT 180

Db 1390 TTGAAGACACTGAATATATACACAGCAGTAGACAGTAGATGATGATTAACCTTAAGGTCAATT 1449
Qy 181 ACCACAGGCCAGGGGCTGGCAGCGTCTCATCATCAACCTTAAGCAGAGAGCTTTGCT 240
Db 1450 ACCACAGGCCAGGGGCTGGCAGCGTCTCATCATCAACCTTAAGCAGAGAGCTTTGCT 1509
Qy 241 TCTCTCTTAATAATGAGTTACCTACATTTTAATGACCGTGAATGTAGATAGTACTATA 300
Db 1510 TCTCTCTTAATAATGAGTTACCTACATTTTAATGACCGTGAATGTAGATAGTACTATA 1569
Qy 301 TGCCGCTACAAAAAGGTAAACCTTTTATATTTTATACATTAACTTCAGCCAGCTATTGA 360
Db 1570 TGCCGCTACAAAAAGGTAAACCTTTTATATTTTATACATTAACTTCAGCCAGCTATTGA 1629
Qy 361 TATATAATAAACATTTTACACACAATACATAAGTTAACTATTATTCTTAATGTGCT 420
Db 1630 TATATAATAAACATTTTACACACAATACATAAGTTAACTATTATTCTTAATGTGCT 1689
Qy 421 AGTCTTTCCCTGCTTAATGAAAAGCTT 448
Db 1690 AGTCTTTCCCTGCTTAATGAAAAGCTT 1717

RESULT 4
AD131633
ID AD131633 standard; cDNA; 1717 BP.

XX AC AD131633;
XX DT 17-JUN-2004 (first entry)

XX DE Human cDNA #959.
XX KW Human; gene; ss; immunological response; immunopathological condition;
KW Crohn's disease; asthma; ulcerative colitis; hypereosinophilia;
KW Irritable bowel syndrome; osteoarthritis; rheumatoid arthritis;
KW acute monocytic leukaemia; antiinflammatory; antiasthmatic; antiulcer;
KW osteopathic; antiarthritic; antirheumatic; cyostatic.

XX OS Homo sapiens.
XX PN US6607879-B1.

XX PD 19-AUG-2003.
XX PF 09-FEB-1998; 98US-00023655.

XX PR 09-FEB-1998; 98US-00023655.
XX PA (INCY-) INCYTE CORP.

XX PI Cocks BG, Stuart SG, Seilhamer JJ;
XX DR WPI; 2003-895307/82.

XX PT A composition comprising a plurality of cDNAs, useful for detecting
PT altered expression of genes in an immunological response or for
PT diagnosing and treating an immunopathology, e.g. Crohn's disease, asthma
PT or osteoarthritis.

XX PS Claim 1; SEQ ID NO 959; 50pp; English.

XX CC The invention relates to a composition comprising a plurality of cDNAs
CC for detecting the altered expression of genes in an immunological
CC response. The invention also relates to a method of diagnosing or
CC monitoring the treatment of an immunopathological condition in a sample,
CC comprising obtaining nucleic acids from a sample, contacting the nucleic
CC acids of the sample with an array comprising the plurality of cDNAs under
CC conditions to form one or more hybridisation complexes, detecting the
CC hybridisation complexes and comparing the levels of the detected
CC hybridisation complexes with the level of hybridisation complexes
CC detected in a non-diseased sample, where an altered level of the detected

CC hybridisation complexes correlates with the presence of an
CC immunopathological condition. Also disclosed are an expression profile
CC comprising a microarray and a plurality of detectable complexes and a
CC method for identifying a plurality of polynucleotide probes. The cDNAs
CC are useful as hybridisable array elements in a microarray for monitoring
CC the expression of target polynucleotides. The microarray can be used in
CC the diagnosis of an immunopathology, such as Crohn's disease, asthma,
CC ulcerative colitis, hypereosinophilia, irritable bowel syndrome,
CC osteoarthritis, rheumatoid arthritis or acute monocytic leukaemia, and in
CC identifying agents for the treatment of the diseases. The microarray may
CC also be used in drug discovery and development, toxicological and
CC carcinogenicity studies, forensics or pharmacogenomics. The composition
CC may also be used in purification of a subpopulation of mRNAs, cDNAs or
CC genomic fragments. This sequence represents a human cDNA of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification but was obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html.

XX SQ Sequence 1717 BP; 434 A; 428 C; 351 G; 504 T; 0 U; 0 Other;

Query Match 100.0%; Score 448; DB 11; Length 1717;
Best Local Similarity 100.0%; Pred. No. 1.4e-104;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TAGGTCAATGCAGAAAATTCCTTAAGAAGAGGACCAAGAGATGAAGCAACACATT 60
Db 1270 TAGGTCAATGCAGAAAATTCCTTAAGAAGAGGACCAAGAGATGAAGCAACACATT 1329

Qy 61 AAGCCTTCACACTCACTCACTTAATAACAGTCTTTCAAACTTCCAGTGCACACTGAAGCTC 120
Db 1330 AAGCCTTCACACTCACTCACTTAATAACAGTCTTTCAAACTTCCAGTGCACACTGAAGCTC 1389

Qy 121 TTGAAGACACTGAATATATACACACAGAGTGGCAGTAGATGATGATACCTTAAGGTCAATT 180
Db 1390 TTGAAGACACTGAATATATACACACAGAGTGGCAGTAGATGATGATACCTTAAGGTCAATT 1449

Qy 181 ACCACAGGCCAGGGGCTGGGACGCTACTCTTCATCAACCTTAAGCAGAGCTTTGCT 240
Db 1450 ACCACAGGCCAGGGGCTGGGACGCTACTCTTCATCAACCTTAAGCAGAGCTTTGCT 1509

Qy 241 TCTCTCTTAATAATGAGTTACCTACATTTTAATGCAACCTGAATGTAGATAGTACTATA 300
Db 1510 TCTCTCTTAATAATGAGTTACCTACATTTTAATGCAACCTGAATGTAGATAGTACTATA 1569

Qy 301 TGCCGCTACAAAAAGGTAAACCTTTTATATTTTATACATTAACTTCAGCCAGCTATTGA 360
Db 1570 TGCCGCTACAAAAAGGTAAACCTTTTATATTTTATACATTAACTTCAGCCAGCTATTGA 1629

Qy 361 TATATAATAAACATTTTACACACAATACATAAGTTAACTATTATTCTTAATGTGCT 420
Db 1630 TATATAATAAACATTTTACACACAATACATAAGTTAACTATTATTCTTAATGTGCT 1689

Qy 421 AGTCTTTCCCTGCTTAATGAAAAGCTT 448
Db 1690 AGTCTTTCCCTGCTTAATGAAAAGCTT 1717

RESULT 5
ADS83700
ID ADS83700 standard; cDNA; 1717 BP.

XX AC ADS83700;

XX DT 11-AUG-2005 (first entry)
XX DE Human lymph node cDNA #959.

XX KW ss; gene; human; immunological response; blood cell; cancer;
KW immunopathological; AIDS; allergy; anaemia; asthma; atherosclerosis;
KW bronchitis; ulcerative colitis; diabetes; multiple sclerosis;
KW osteoporosis; pancreatitis; infection; arthritis; lymph node.

XX OS Homo sapiens.

Db 1547 TTGAGACACTGAAATATACACAGCAGTAGAGATGCAATGTAACCTTAAGTCAATT 1606
QY 181 ACCACAGGCCAGGGGCTGGGACGCGTACTCATCATCAACCCCTAAAGACAGAGCTTTGCT 240
Db 1607 ACCACAGGCCAGGGGCTGGGACGCGTACTCATCATCAACCCCTAAAGACAGAGCTTTGCT 1666
QY 241 TCTCTCTCTAAATGAGTTACCTACATTTTAATGACACCTGAATGTTAGATAGTACTATA 300
Db 1667 TCTCTCTCTAAATGAGTTACCTACATTTTAATGACACCTGAATGTTAGATAGTACTATA 1726
QY 301 TGGCGCTACAAAAAGGTAAACCTTTTATATTTTATACATTAATTCAAGCCAGCTATTGA 360
Db 1727 TGGCGCTACAAAAAGGTAAACCTTTTATATTTTATACATTAATTCAAGCCAGCTATTGA 1786
QY 361 TATAAATAAAACATTTTCACACACAATAAAGTTAACTATTATTATTTCTAATGTGCT 420
Db 1787 TATAAATAAAACATTTTCACACACAATAAAGTTAACTATTATTATTTCTAATGTGCT 1846
QY 421 AGTTCTTTCCCTGCTTAATGAAAAGCTT 448
Db 1847 AGTTCTTTCCCTGCTTAATGAAAAGCTT 1874

RESULT 7
ADC03342
ID ADC03342 standard; cDNA; 1915 BP.
XX AC ADC03342;
XX DT 18-DEC-2003 (first entry)
XX DE Human cDNA encoding chemokine receptor 88-2B.
XX 88; gene; human; anti-HIV; virucide; HIV; SIV; 88-C; 88-2B;
KW chemokine receptor; envelope protein; atherosclerosis;
KW rheumatoid arthritis; tumour growth suppression; asthma; viral infection;
KW AIDS; inflammatory condition; chromosome 3p21.
XX OS Homo sapiens.
XX Key location/Qualifiers
FH CDS 362..1429
FT /*tag= a
FT /product= "Chemokine receptor 88-C"
FT /note= "This CDS, minus the STOP codon, is specifically
FT claimed in claim 11"

XX PN US2002150888-A1.
XX PD 17-OCT-2002.
XX PF 26-MAR-2002; 2002US-00106623.
XX PR 20-DEC-1995; 95US-00575967.
PR 07-JUN-1996; 96US-00661393.
PR 20-DEC-1996; 96US-00771276.
XX PA (GRAY/) GRAY P W.
PA (SCHW/) SCHWEICKART V L.
PA (RAPO/) RAPORT C J.
XX PI Gray PW, Schweickart VL, Raport CJ;
XX DR WPI; 2003-182491/18.
DR P-PSDB; ADC03343.
XX
PT Screening for a modulator of HIV and SIV infection utilizing
PT polynucleotides that encode the 88C or 88-2B chemokine receptors, useful
PT for diagnosing and treating disorders such as atherosclerosis, arthritis,
PT AIDS and asthma.
XX
PS Claim 11; Page 18-20; 29pp; English.

XX The invention relates to screening for a modulator of human
CC immunodeficiency virus (HIV) or simian immunodeficiency virus (SIV)
CC infection, comprising contacting a first composition having an human
CC (ADC03341) or macaque (ADC03359) 88C chemokine receptor polypeptide with
CC a second composition having an HIV or SIV envelope protein in the
CC presence or absence of a compound. Also included are screening for a
CC modulator of HIV infection, detecting HIV infection of cells (comprising
CC contacting a cell that has been recombinantly modified to express at
CC least one of human chemokine receptors 88C and 88-2B with HIV, and
CC detecting HIV infection in the cell) and inhibiting HIV infection of
CC cells (comprising contacting cells with an antibody to at least one of
CC human chemokine receptors 88C and 88-2B with HIV, and detecting HIV
CC infection of the cell after the contacting step). The methods and
CC compositions of the present invention are useful for the diagnosis and
CC treatment of disorders associated with the aberrant expression or
CC activity of 88C or 88-2B chemokine receptors, such as atherosclerosis,
CC rheumatoid arthritis, tumour growth suppression, asthma, viral infection,
CC AIDS and other inflammatory conditions. The genes for human 88-C and 88-
CC 2B are located on chromosome 3p21. The present sequence encodes human
CC chemokine receptor 88-2B.
XX
SQ Sequence 1915 BP; 488 A; 470 C; 373 G; 584 T; 0 U; 0 Other;

Query Match 100.0%; Score 448; DB 10; Length 1915;
Best Local Similarity 100.0%; Pred. No. 1.5e-104;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAGGTGAGATGCGAAGAAATGGCTTAAGAGGAAAGGACCAAGAGATGAAGCAACACATT 60
Db 1427 TAGGTGAGATGCGAAGAAATGGCTTAAGAGGAAAGGACCAAGAGATGAAGCAACATT 1486
QY 61 AAGCTTCCACACTCACTCACTTAAACAGTCTTCAAACTTCCAGTGCAACACTGAAGCTC 120
Db 1487 AAGCTTCCACACTCACTCACTTAAACAGTCTTCAAACTTCCAGTGCAACACTGAAGCTC 1546
QY 121 TTGAAGACACTGAAATATACACACAGCAGTGGCAGTAGATGCATGTAACCTAAGTCAATT 180
Db 1547 TTGAAGACACTGAAATATACACACAGCAGTGGCAGTAGATGCATGTAACCTAAGTCAATT 1606
QY 181 ACCACAGGCCAGGGGCTGGGACGCGTACTCATCATCAACCTTAAAGACAGAGCTTTGCT 240
Db 1607 ACCACAGGCCAGGGGCTGGGACGCGTACTCATCATCAACCTTAAAGACAGAGCTTTGCT 1666
QY 241 TCTCTCTCTAAATGAGTTACCTACATTTTAATGACCTGAATGTTAGATAGTACTATA 300
Db 1667 TCTCTCTCTAAATGAGTTACCTACATTTTAATGACCTGAATGTTAGATAGTACTATA 1726
QY 301 TGGCGCTACAAAAAGGTAAACCTTTTATATTTTATACATTAACCTCAGCCAGCTATTGA 360
Db 1727 TGGCGCTACAAAAAGGTAAACCTTTTATATTTTATACATTAACCTCAGCCAGCTATTGA 1786
QY 361 TATAAATAAAACATTTTCACACACAATAAAGTTAACTATTATTCTAATGTGCT 420
Db 1787 TATAAATAAAACATTTTCACACACAATAAAGTTAACTATTATTCTAATGTGCT 1846
QY 421 AGTTCTTTCCCTGCTTAATGAAAAGCTT 448
Db 1847 AGTTCTTTCCCTGCTTAATGAAAAGCTT 1874

RESULT 8
ADT90848
ID ADT90848 standard; cDNA; 1915 BP.
XX
AC ADT90848;
XX
DT 16-DEC-2004 (first entry)
XX
DE Human chemokine receptor 88-2B cDNA.
XX
KW Chemokine receptor 88C; chemokine receptor 88-2B;
KW human immunodeficiency virus; simian immunodeficiency virus; HIV; SIV;

Sequence	Location/Qualifiers
Sequence 1915 BP; 488 A; 470 C; 373 G; 584 T; 0 U; 0 Other;	
XX	infection; vaccine; virucide; gene; ss.
XX	Homo sapiens.
XX	
PH	Key
FT	5'UTR
FT	1..361
FT	/*tag= a
FT	362..1429
FT	/*tag= c
FT	/product= "Human chemokine receptor 88-2B protein"
FT	362..469
FT	/*tag= b
FT	/note= "Encodes extracellular domain"
FT	539..574
FT	/*tag= d
FT	/note= "Encodes extracellular domain"
FT	638..682
FT	/*tag= e
FT	/note= "Encodes intracellular domain"
FT	752..814
FT	/*tag= f
FT	/note= "Encodes intracellular domain"
FT	872..949
FT	/*tag= g
FT	/note= "Encodes extracellular domain"
FT	1016..1081
FT	/*tag= h
FT	/note= "Encodes extracellular domain"
FT	1148..1213
FT	/*tag= i
FT	/note= "Encodes intracellular domain"
FT	1277..1426
FT	/*tag= j
FT	/note= "Encodes intracellular domain"
FT	1430..1915
FT	/*tag= k
XX	
PN	US6797811-B1.
XX	
PD	28-SEP-2004.
XX	
XX	20-DEC-1996; 96US-00771276.
PF	
XX	
PR	20-DEC-1995; 95US-00575967.
PR	07-JUN-1996; 96US-00661393.
XX	
PA	(ICOS-) ICOS CORP.
XX	
PI	Gray PW, Schweickart VL, Raport CJ;
XX	
DR	WPI; 2004-687775/67.
DR	P-PSDB; ADT90849.
XX	
PT	New antibodies specifically binding to (the extracellular domain of) a
PT	chemokine receptor 88C polypeptide expressed on the surface of cells,
PT	useful for inhibiting human or simian human immunodeficiency infection of
PT	such cells.
XX	
PS	Example 2; SEQ ID NO 3; 29pp; English.
XX	
CC	The invention relates to a novel antibody that specifically binds to the
CC	extracellular domain of a chemokine receptor 88C or 88-2B polypeptide
CC	expressed on the surface of cells. The antibody fails to cross-react with
CC	an MCP-1 receptor (CCCKR-2) and is useful for inhibiting human or simian
CC	immunodeficiency virus (HIV or SIV) infection of the cells expressing
CC	chemokine receptor 88C or 88-2B. The invention is also used to detect 88C
CC	or 88-2B gene products their analogues or biologically active fragments.
CC	The antibody products may be used to as modulators of receptor activities
CC	or to diagnose tissue-specific variations in expression of 88-2B or 88C.
CC	The invention is also used in the preparation of vaccines. The present
CC	sequence is the human chemokine receptor 88-2B cDNA.
XX	

Query Match	100.0%;	Score 448;	DB 13;	Length 1915;
Best Local Similarity	100.0%;	Pred. No. 1.5e-104;		
Matches 448;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY 1	TAGTCAGATGCAGAAATTGCCTAAAGAGGAGGACCAGAGATGAGCAACACATT	60		
DB 1427	TAGTCAGATGCAGAAATTGCCTAAAGAGGAGGACCAGAGATGAGCAACACATT	1486		
QY 61	AAGCCTTCCACACTCACTCTTAAACAGTCCCTGAACTTCCAGTGCAACACTGAACTC	120		
DB 1487	AAGCCTTCCACACTCACTCTTAAACAGTCCCTGAACTTCCAGTGCAACACTGAACTC	1546		
QY 121	TTGAAGACACTGAAATATACACACAGCAGTAGCAGTAGATGCATGTACCCTAAGGTCAAT	180		
DB 1547	TTGAAGACACTGAAATATACACACAGCAGTAGCAGTAGATGCATGTACCCTAAGGTCAAT	1606		
QY 181	ACCA CAGGCCAGGGGCTGGG CAGCGTACTCATCATCAACCTTAAAAAGCAGAGCTTTGCT	240		
DB 1607	ACCA CAGGCCAGGGGCTGGG CAGCGTACTCATCATCAACCTTAAAAAGCAGAGCTTTGCT	1666		
QY 241	TCTCTCTTAAATGAATTACCTACATTTTAATGCACTGAAATGTTAGATAGTTACTATA	300		
DB 1667	TCTCTCTTAAATGAATTACCTACATTTTAATGCACTGAAATGTTAGATAGTTACTATA	1726		
QY 301	TGCCGCTACAAAAAGGTAAAACTTTTATATTTTTATACATTTAATCTTACGCCAGCTATTGA	360		
DB 1727	TGCCGCTACAAAAAGGTAAAACTTTTATATTTTTATACATTTAATCTTACGCCAGCTATTGA	1786		
QY 361	TATAAATAAAACATTTTACACAATATACAATAAGTTAACTATTATTCTAATGTGCT	420		
DB 1787	TATAAATAAAACATTTTACACAATATACAATAAGTTAACTATTATTCTAATGTGCT	1846		
QY 421	AGTTCTTTCCCTGCTTAATGAAAAGCTT 448			
DB 1847	AGTTCTTTCCCTGCTTAATGAAAAGCTT 1874			

RESULT	9
ID	ADU47727
AC	ADU47727 standard; CDNA; 1915 BP.
XX	
XX	ADU47727;
DT	10-FEB-2005 (first entry)
DE	Human chemokine receptor 88-2B cDNA.
XX	
KW	Chemokine receptor; 88C; human immunodeficiency virus;
KW	simian immunodeficiency virus; HIV; SIV; MCP-1; CCRK-2; 88-2B;
KW	leukocyte trafficking; acquired immune deficiency syndrome; AIDS;
KW	psoriasis; rheumatoid arthritis; atherosclerosis; tumour; asthma;
KW	viral infection; inflammation; anti-HIV; virucide; antipsoriatic;
KW	antiarthritic; arteriosclerotic; antiinflammatory; human; gene; ss.
OS	Homo sapiens.
XX	
XX	
FH	Key
FT	5'UTR
FT	Location/Qualifiers
FT	1..361
FT	/tag= a
CDS	362..1429
FT	/tag= b
FT	/product= "Chemokine receptor 88-2B "
FT	1430..1915
FT	/tag= c
PN	US2004230037-A1.
PD	18-NOV-2004.
XX	
PF	04-FEB-2004; 2004US-00772037.
XX	
PR	20-DEC-1995; 95US-00575967.

Db 4652 TAGGTGAGATGCAGAAAATTGCTTAAGAAGAGGACCAAGGAGATGAAGCAAAACACATT 4711
Qy 61 AAGCTTCCACACTCACCCTTAATAAGAGTCCCTCAAACTTCCAGTGCACACACTGAAGCTC 120
Db 4712 AAGCCTTCCACACTCACCCTTAATAAGAGTCCCTCAAACTTCCAGTGCACACACTGAAGCTC 4771
Qy 121 TTGAAGACACTGAAATATACACACAGCAGTAGCAGTAGAGATGATGCCCTAAGGTCATT 180
Db 4772 TTGAAGACACTGAAATATACACACAGCAGTAGCAGTAGAGATGATGCCCTAAGGTCATT 4831
Qy 181 ACCACAGGCCAGGGGCTGGGCGACGCTACTCATCATCAACCCCTAAAGACAGAGCTTGGCT 240
Db 4832 ACCACAGGCCAGGGGCTGGGCGACGCTACTCATCATCAACCCCTAAAGACAGAGCTTGGCT 4891
Qy 241 TCTCTCTTAATAATGAGTTACCTACATTTTAATGCACCTGAATGTTAGATAGTTACTATA 300
Db 4892 TCTCTCTTAATAATGAGTTACCTACATTTTAATGCACCTGAATGTTAGATAGTTACTATA 4951
Qy 301 TGCCGCTACAAAAAGGTAAACTTTTATATTATATTATACATTAACTTCAGCCAGCTATTGA 360
Db 4952 TGCCGCTACAAAAAGGTAAACTTTTATATTATATTATACATTAACTTCAGCCAGCTATTGA 5011
Qy 361 TATAAATAAAACATTTTACACACAATAAAGTTAACTATTATTCTAATGTGCTT 420
Db 5012 TATAAATAAAACATTTTACACACAATAAAGTTAACTATTATTCTAATGTGCTT 5071
Qy 421 AGTTCTTCCCTGCTTAATGAAGCTT 448
Db 5072 AGTTCTTCCCTGCTTAATGAAGCTT 5099

RESULT 11

ABZ68879
ID ABZ68879 standard; cDNA; 5791 BP.

XX AC ABZ68879;

XX DT 28-MAY-2003 (first entry)

XX DE Nucleotide sequence of human chemokine receptor CCR3.

XX KW Human; chemokine receptor; CCR3; viral infection; surface protein;
KW respiratory virus infection; respiratory syncytial virus infection;
KW RSV infection; bronchiolitis; pneumonia; asthma; gene; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT CDS 4015..5082

FT /*tag= a

FT /product= "CCR3"

XX PN W02003014153-A2.

XX PD 20-FEB-2003.

XX PF 12-AUG-2002; 2002WO-CA001248.

XX PR 10-AUG-2001; 2001US-0311088P.

XX PA (TOPI-) TOPIGEN PHARM INC.

XX PI Renzi P, Zenzoumi K;

XX DR WPI; 2003-256541/25.

XX DR P-PSDB; ABP97726.

XX PT Modulating viral infection of a cell, for treating or preventing
XX PT respiratory virus infections, bronchitis, pneumonia or asthma, by
XX PT modulating a binding interaction between a cell chemokine-receptor and a
XX PT surface protein of the virus.

XX PS Disclosure; Page 84-88; 120pp; English.

XX CC The present sequence encodes human chemokine receptor CCR3. The
CC specification describes a method for modulating viral infection of a
CC cell. The method comprises modulating a binding interaction between a
CC cell chemokine-receptor and a surface protein of the virus. The proviso
CC is that the cell chemokine-receptor is not CX3CR1 and that the virus is
CC not HIV. The method is useful for treating or preventing respiratory
CC virus infection in vertebrates, more particularly respiratory syncytial
CC virus (RSV) infections, and related diseases, e.g. bronchiolitis,
CC bronchitis, pneumonia or asthma
XX SQ Sequence 5791 BP; 1624 A; 1285 C; 1160 G; 1722 T; 0 U; 0 Other;

Query Match 100.0%; Score 448; DB 8; Length 5791;

Best Local Similarity 100.0%; Pred. No. 2e-104;

Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TAGGTGAGATGCAGAAAATTGCTTAAGAAGAGGACCAAGGAGATGAAGCAAAACACATT 60
Db 5080 TAGGTGAGATGCAGAAAATTGCTTAAGAAGAGGACCAAGGAGATGAAGCAAAACACATT 5139
Qy 61 AAGCCTTCCACACTCACCCTTAATAAGAGTCCCTCAAACTTCCAGTGCACACACTGAAGCTC 120
Db 5140 AAGCCTTCCACACTCACCCTTAATAAGAGTCCCTCAAACTTCCAGTGCACACACTGAAGCTC 5199
Qy 121 TTGAAGACACTGAAATATACACACAGCAGTAGCAGTAGAGATGATGCCCTAAGGTCATT 180
Db 5200 TTGAAGACACTGAAATATACACACAGCAGTAGCAGTAGAGATGATGCCCTAAGGTCATT 5259
Qy 181 ACCACAGGCCAGGGGCTGGGCGACGCTACTCATCATCAACCCCTAAAGACAGAGCTTGGCT 240
Db 5260 ACCACAGGCCAGGGGCTGGGCGACGCTACTCATCATCAACCCCTAAAGACAGAGCTTGGCT 5319
Qy 241 TCTCTCTTAATAATGAGTTACCTACATTTTAATGCACCTGAATGTTAGATAGTTACTATA 300
Db 5320 TCTCTCTTAATAATGAGTTACCTACATTTTAATGCACCTGAATGTTAGATAGTTACTATA 5379
Qy 301 TGCCGCTACAAAAAGGTAAACTTTTATATTATATTATACATTAACTTCAGCCAGCTATTGA 360
Db 5380 TGCCGCTACAAAAAGGTAAACTTTTATATTATATTATACATTAACTTCAGCCAGCTATTGA 5439
Qy 361 TATAAATAAAACATTTTACACACAATAAAGTTAACTATTATTCTAATGTGCTT 420
Db 5440 TATAAATAAAACATTTTACACACAATAAAGTTAACTATTATTCTAATGTGCTT 5499
Qy 421 AGTTCTTCCCTGCTTAATGAAGCTT 448
Db 5500 AGTTCTTCCCTGCTTAATGAAGCTT 5527

RESULT 12

ADY86631
ID ADY86631 standard; DNA; 5791 BP.

XX AC ADY86631;

XX DT 02-JUN-2005 (first entry)

XX DE Human CC chemokine receptor 3 (CCR3) gene.

XX KW Gene expression; screening; multiple sclerosis; neuroprotective;
KW immune disorder; neurological disease; DNA microarray; gene; ds;
KW chemokine.

XX OS Homo sapiens.

XX PN US2005064483-A1.

XX PD 24-MAR-2005.

XX PF 30-AUG-2004; 2004US-00929182.

XX PR 28-AUG-2003; 2003US-0498731P.

Db 1430 AGGCCA-GGGCTGGCAGCGTACATCATCAA-CCTAAAGACAGAGCTTGTCTCT 1487
QY 246 CTCTAAATGAGTTACCTACATTTTAATGCACCTGAATGTAGATAGTACTATATGCCG 305
Db 1488 CTCTAAATGAGTTACCTATATTTTAATGCACCTGAATGTAGATAGTACTATATGCCG 1547
QY 306 CTACAAAAAGGTAAACCTTTTATATTTTATACATTACTTCAGCCAGCTATTGATATTA 365
Db 1548 CTACAAAAAGGTAAACCTTTTATATTTTATACATTACTTCAGCCAGCTATT-ATAATA 1606
QY 366 ATAAACATTTTCACACAAATACATAAGTTAACTATTCTTCTAATGTGCTAGTTC 425
Db 1607 ATAAACATTTTCACACAAATACATAAGTTAACTATTCTTCTAATGTGCTAGTTC 1666
QY 426 TTTCCTGCTTAATGAAAAGCTT 448
Db 1667 TTTCCTGCTTAATGAAAAGCTT 1689

RESULT 14
AAT58783
ID AAT58783 standard; DNA; 1689 BP.
AC AAT58783;
XX
DT 30-SEP-1997 (first entry)
XX
DE Human C-C chemokine receptor 3 DNA.
XX
KW Human; eotaxin; eosinophil; chemoattractant; stimulation; accumulation; attraction; chemotaxis; diagnosis; prevention; treatment; disease;
KW inflammation; allergy; asthma; rhinitis; hypersensitivity; lung;
KW pneumonia; Loeffler's; syndrome; interstitial; ILD;
KW idiopathic pulmonary fibrosis; rheumatoid arthritis; systemic;
KW lupus erythematosus; SLR; ankylosing spondylitis; sclerosis; Sjorgen's;
KW polymyositis; dermatomyositis; bowel; anaphylaxis; drug; penicillin;
KW cephalosporin; insect sting; Crohn's; ulcerative colitis;
KW spondyloarthropathy; scleroderma; psoriasis; dermatosis; dermatitis;
KW eczema; atopic; urticaria; necrotizing; cutaneous; vasculitis; myositis;
KW fascitis; multiple sclerosis; myasthenia gravis; juvenile onset diabetes;
KW glomerulonephritis; autoimmune; thyroiditis; Bechet's; graft; rejection;
KW transplantation; allograft; graft versus host; cancer;
KW leukocyte infiltration; reperfusion injury; atherosclerosis;
KW haematologic malignancy; septic; endotoxic; shock; polymyositis;
KW dermatomyositis; immunosuppression; immunodeficiency; AIDS;
KW radiation therapy; chemotherapy; autoimmune; corticosteroid;
KW C-C chemokine receptor 3; CRK3; ss.
XX
OS Homo sapiens.

XX
FH Key Location/Qualifiers
FT CDS 181..1248
FT /*tag= a
FT /product= "CRK3"
XX
PN WO9700960-A1.
XX
PD 09-JAN-1997.
XX
XX 21-JUN-1996; 96WO-US010723.
XX
XX 23-JUN-1995; 95US-00494093.
XX
PA (LEUK-) LEUKOSITE INC.
XX
PI Ponath PD, Qin S, Ringler DJ, Newman W, Mackay C;
XX
XX WPI; 1997-087387/08.
DR P-PSDB; AAM10100.
XX
PT New isolated human eotaxin gene - used to develop prods. for the
PT diagnosis and treatment of e.g. inflammation, allergies, auto-immune

PT disease, infections and tumours.
XX
PS Example 7; Page 97; 130pp; English.

XX The present sequence encodes human C-C chemokine receptor 3 (CRK3), to
CC which human eotaxin (hE), an eosinophil specific chemoattractant capable
CC of stimulating eosinophil accumulation and/or attracting eosinophils
CC (including chemotaxis), binds. hE can be used to develop products for the
CC diagnosis, prevention or treatment of hE associated diseases or
CC conditions. The products can be used to treat inflammatory or allergic
CC diseases and conditions, including respiratory allergic diseases (e.g.
CC asthma, allergic rhinitis, hypersensitivity lung diseases or pneumonitis,
CC eosinophilic pneumonia, interstitial lung diseases (ILD) such as
CC eosinophilic pneumonia, interstitial lung diseases (ILD) such as
CC idiopathic pulmonary fibrosis or ILD associated with rheumatoid
CC arthritis, systemic lupus erythematosus (SLE), ankylosing spondylitis,
CC systemic sclerosis, Sjorgen's syndrome, polymyositis or dermatomyositis),
CC to penicillin and cephalosporins), insect sting allergies, inflammatory
CC bowel diseases (e.g. Crohn's disease and ulcerative colitis),
CC spondyloarthropathies, scleroderma, psoriasis and inflammatory dermatoses
CC (e.g. dermatitis, eczema, atopic dermatitis, allergic contact dermatitis,
CC urticaria and necrotizing, cutaneous and hypersensitivity vasculitis),
CC eosinophilic myositis and fascitis, multiple sclerosis, SLE, myasthenia
CC gravis, juvenile onset diabetes, glomerulonephritis, autoimmune
CC thyroiditis, Bechet's disease, graft rejection (e.g. in transplantation)
CC including allograft rejection or graft versus host disease and cancers
CC with leukocyte infiltration of the skin or organs. The products can also
CC be used to treat other diseases or conditions requiring the inhibition of
CC undesirable inflammatory responses, including reperfusion injury,
CC atherosclerosis, certain haematologic malignancies, cytokine induced
CC toxicity (e.g. septic or endotoxic shock), polymyositis, dermatomyositis,
CC immunosuppression (e.g. in individuals with immunodeficiency syndromes
CC such as AIDS, undergoing radiation therapy, chemotherapy, therapy for
CC autoimmune disease or other drug therapy, such as corticosteroid therapy,
CC which causes immunosuppression), immunosuppression due to (e.g.
CC congenital) deficiency (e.g. in eotaxin) or infectious diseases such as
CC parasitic diseases. Degenerate primers based on the guinea pig eotaxin
CC amino acid sequence were used for the reverse transcriptase polymerase
CC chain reaction (RT-PCR) amplification of RNA isolated from inflamed,
CC eosinophilic lung tissue obtained from Balb/c mice sensitised to
CC ovalbumin. The amplification product was used as a probe to screen a
CC human genomic library in vector EMBL3 9P6/T7 to obtain the hE gene
XX
SQ Sequence 1689 BP; 431 A; 416 C; 344 G; 497 T; 0 U; 1 Other;

Query Match 84.9%; Score 380.4; DB 2; Length 1689;
Best Local Similarity 98.4%; Pred. No. 2.9e-87;
Matches 436; Conservative 0; Mismatches 2; Indels 5; Gaps 5;

QY 7 AGATGCAAAAAATTGGCTTAAGAGGAGCAAGAGATGAAACAACATTAAAGCT 66
Db 1251 AGATGCAAAAAATTGGCTTAAGAGGAGCAAGAGATGAAACAACATTAAAGCT 1310
QY 67 TCCACACTCACCTCTAAACAGTCTTCAAA-CTTCCAGTCAACACTGAAGCTCTGAA 125
Db 1311 TCCACACTCACCTCTAAACAGTCTTCAAACTTCCAGTCAACACTGAAGCTCTT-AA 1369
QY 126 GACACTGAATATATACACACAGCAGTAGACATGATGATGATCCCTAAGCTATTACCAC 185
Db 1370 GACACTGAATATATACACACAGCAGTAGACATGATGATGATCCCTAAGCTATTACCAC 1429
QY 186 AGGCCAGGGGCTGGGCGACGGTACTCATCATCAACCCTAAGAGAGAGCTTGTCTCT 245
Db 1430 AGGCCA-GGGCTGGGCGACGGTACTCATCATCAACCCTAAGAGAGAGCTTGTCTCT 1487
QY 246 CTCTAAATGAGTTACCTACATTTTAAATGCACCTGAATGTAGATAGTACTATATGCCG 305
Db 1488 CTCTAAATGAGTTACCTATATTTTAAATGCACCTGAATGTAGATAGTACTATATGCCG 1547
QY 306 CTACAAAAAGGTAAACCTTTTATATTTTATACATTACTTCAGCCAGCTATTGATATTA 365
Db 1548 CTACAAAAAGGTAAACCTTTTATATTTTATACATTACTTCAGCCAGCTATT-ATAATA 1606

QY 366 ATAAACATTTTCACACAATAAAGTTACTATTCTTAATGTCCTAGTTC 425
|||||
Db 1607 ATAAACATTTTCACACAATAAAGTTACTATTCTTAATGTCCTAGTTC 1666
QY 426 TTTCCTGCTTAATGAAGCTT 448
|||||
Db 1667 TTTCCTGCTTAATGAAGCTT 1689

RESULT 15
AAV07402 standard; DNA; 1689 BP.
AC AAV07402;
DT 28-SEP-1998 (first entry)
DE Human C-C chemokine receptor 3 genomic DNA.
XX
KW C-C chemokine receptor 3; CCR3; Eos I2; human;
KW G protein-coupled receptor; leukocyte; antibody; antagonist;
KW inflammation; allergy; asthma; graft rejection; infection;
KW autoimmune disease; drug screening; therapy; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 181..1248
FT /*tag= a
FT
XX
PN WO9814480-A1.
XX
PD 09-APR-1998.
XX
PF 24-SEP-1997; 97WO-US017103.
XX
PR 30-SEP-1996; 96US-00720565.
XX
PA (LEUK-) LEUKOSITE INC.
XX
PI Mackay CR, Ponath PD;
XX
XX WPI; 1998-286418/25.
DR P-PSDB; AAM51744.
XX
XX
PT Antibodies to chemokine receptor-3 protein - useful for diagnosis and
PT treatment of inflammatory conditions, e.g. allergy, asthma, autoimmune
PT disease, graft rejection or cancer.
XX
XX
PS Example 2; Fig 1A-C; 185pp; English.
XX
XX This genomic DNA codes for novel human C-C chemokine receptor 3 (see
CC AAM51744), also designated CCR-3, CCR3 or Eos I2, that binds and mediates
CC chemotaxis in response to chemokines such as eotaxin, RANTES and MCP-3.
CC The DNA was isolated from a human genomic phage library using as probe a
CC PCR fragment that had been generated from eosinophil cDNA using primers
CC (see AAV07405-12) based on known chemokine receptor genes. A cDNA clone
CC (see AAV07403) for CCR-3 is also provided. Comparison of the sequences
CC suggests that the genomic DNA has an intron that separates the promoter
CC and most of the 5' untranslated region from the coding region. A
CC consensus of the genomic and cDNA sequences is provided (see AAV07404).
CC The invention relates to isolated and/or recombinant nucleic acids
CC encoding CCR-3, isolated or recombinant CCR-3 polypeptides, recombinant
CC nucleic acid constructs, host cells useful for production of recombinant
CC CCR-3 proteins, to antibodies reactive with the receptors, and to methods
CC of using these products to identify ligands, antagonists and agonists of
CC receptor function. Inhibitors of CCR-3 can be used to treat: inflammatory
CC or allergic diseases and conditions, including respiratory allergic
CC diseases such as asthma, allergic rhinitis, hypersensitivity lung
CC disease, hypersensitivity pneumonitis, eosinophilic pneumonia (e.g.
CC Loeffler's syndrome, chronic eosinophilic pneumonia, interstitial lung
CC disease (ILD) e.g. idiopathic pulmonary fibrosis or ILD associated with

CC rheumatoid arthritis, systemic lupus erythematosus, ankylosing
CC spondylitis, systemic sclerosis, Sjogren's syndrome, polymyositis or
CC dermatomyositis), systemic anaphylaxis or hypersensitivity responses, as
CC drug allergy, insect sting allergy, inflammatory bowel disease, such as
CC Crohn's disease and ulcerative colitis, spondyloarthropathy, scleroderma,
CC psoriasis, inflammatory dermatosis such as dermatitis, eczema, atopic
CC dermatitis, allergic contact dermatitis, urticaria, vasculitis (e.g.
CC necrotizing, cutaneous and hypersensitivity vasculitis); eosinophilic
CC myositis and eosinophilic fasciitis; autoimmune diseases such as
CC rheumatoid arthritis, psoriatic arthritis, multiple sclerosis, systemic
CC lupus erythematosus, myasthenia gravis, juvenile onset diabetes, graft
CC glomerulonephritis, autoimmune thyroiditis and Behcet's disease; graft
CC rejection, including allograft rejection or graft-versus-host disease;
CC cancers with leukocyte infiltration of the skin or organs; and also
CC reperfusion injury, atherosclerosis, certain haematologic malignancies,
CC septic shock and endotoxic shock. Promoters of CCR-3 function can be used
CC for treating: immunosuppression e.g. in AIDS patients or individuals
CC undergoing radiation therapy, chemotherapy, therapy for autoimmune
CC disease or other drug therapy, and immunosuppression due congenital
CC deficiency in receptor function or other causes; and infectious diseases
CC such as parasitic diseases, including helminth infections, such as
CC nematodes (round worms). The agents can also be used for detection and
CC diagnosis
XX
SQ Sequence 1689 BP; 431 A; 416 C; 344 G; 497 T; 0 U; 1 Other;

Query Match 84.9%; Score 380.4; DB 2; Length 1689;
Best Local Similarity 98.4%; Pred. No. 2.9e-87;
Matches 436; Conservative 0; Mismatches 2; Indels 5; Gaps 5;

QY 7 AGATGCAGAAAATTGCTTAAGAAGACCAAGAGATGAAGCAACACATTAAAGCT 66
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QY 67 TCACACTCACCTCTAACAAGTCCTTCAA-CTTCAGTGCAACACTGAAGCTTGGAA 125
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QY 126 GACACTGAATATACACACAGCAGTAGCAGTAGATGCATGTACCCTAAGTCATTACAC 185
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QY 186 AGGCCAGGGGCTGGGCGAGCGTATCATCATCAACCCCTAATAAAGCAGAGCTTGGCTTCT 245
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Db 1430 AGGCCA-GGGCTGGGCGAGCGTATCATCATCA-CCTAATAAAGCAGAGCTTGGCTTCTCT 1487

QY 246 CTCTAAATGAGTTACCTACATTTTAATGCACTGAATGTTAGATAGTTACTATATGCGG 305
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QY 366 ATAAACATTTTCACACAATAAAGTTAACTATTCTTAATGTCCTAGTTC 425
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QY 426 TTTCCTGCTTAATGAAGCTT 448
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Db 1667 TTTCCTGCTTAATGAAGCTT 1689

Search completed: January 7, 2006, 07:04:58
Job time : 246.515 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 7, 2006, 05:41:27 ; Search time 2207.58 Seconds
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Title: US-10-767-521-4

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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	448	100.0	448	6	AR164121	AR164121 Sequence
2	448	100.0	448	6	BD128571	BD128571 Bosinophl
3	448	100.0	448	6	AX030931	AX030931 Sequence
4	448	100.0	1717	6	AR380414	AR380414 Sequence
5	448	100.0	1717	6	AX334894	AX334894 Sequence
6	448	100.0	1717	8	HSU51241	U51241 Human eosin
7	448	100.0	1915	6	AR584940	AR584940 Sequence
8	448	100.0	1915	6	BD06761	BD06761 Chemokine
9	448	100.0	1915	6	BD017703	BD017703 Chemokine
10	448	100.0	5791	6	AX705064	AX705064 Sequence
11	448	100.0	5791	8	AF247361	AF247361 Homo sapi
12	448	100.0	177334	8	AC138069	AC138069 Homo sapi
13	448	100.0	197279	8	AC104439	AC104439 Homo sapi
14	448	100.0	220965	14	HSA12688	AJ312688 Homo sapi
15	385	85.9	1913	8	AK123050	AK123050 Homo sapi
16	380.4	84.9	1689	6	BD082060	BD082060 G-protein
17	380.4	84.9	1689	6	AR300121	AR300121 Sequence
18	380.4	84.9	1689	6	AR475065	AR475065 Sequence

19	380.4	84.9	1689	6	AR591370	AR591370 Sequence
20	380.4	84.9	1689	8	HSU49727	U49727 Human C-C c
21	339.2	75.7	7201	6	AX345239	AX345239 Sequence
22	294.4	65.7	7201	6	AX345238	AX345238 Sequence
23	178.6	39.9	144233	4	AP006435	AP006435 Sus scrofa
24	178.6	39.9	167298	4	AP006436	AP006436 Sus scrofa
25	155.4	34.7	1678	4	AB119270	AB119270 Sus scrofa
26	155.4	34.7	1838	4	AB119269	AB119269 Sus scrofa
27	118.4	26.4	816	10	BV208413	BV208413 CCR3 515
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32	105	23.4	1201	6	CS035919	CS035919 Sequence
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35	105	23.4	1201	6	CS129103	CS129103 Sequence
36	105	23.4	1201	6	AR270522	AR270522 Sequence
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38	105	23.4	1201	6	AX548778	AX548778 Sequence
39	105	23.4	1201	8	HSU28694	U28694 Human eosin
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41	56.2	12.5	1440	9	MMU28406	U28406 Mus musculu
42	50.6	11.3	164233	5	CR752649	CR752649 Zebrafish
43	48.4	10.8	349980	6	AX344574	AX344574 Sequence
44	48.2	10.8	348034	2	CR382400	CR382400 Plasmidiu
45	47.4	10.6	168406	14	AC090770	AC090770 Homo sapi

ALIGNMENTS

RESULT 1
AR164121
LOCUS AR164121 448 bp
DEFINITION Sequence 4 from patent US 6271347.
ACCESSION AR164121
VERSION AR164121.1 GI:16235067
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 448)
AUTHORS Daugherty,B.L., Demartino,J.A., Siciliano,S.J. and Springer,M.S.
TITLES Bosinophl eotaxin receptor
JOURNAL Patent: US 6271347-A 4 07-AUG-2001;
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source location/Qualifiers
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DB	61	100.0%	448	6	448	448	0	0	0	0
QY	121	100.0%	448	6	448	448	0	0	0	0
DB	121	100.0%	448	6	448	448	0	0	0	0
QY	181	100.0%	448	6	448	448	0	0	0	0
DB	181	100.0%	448	6	448	448	0	0	0	0
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DB	241	100.0%	448	6	448	448	0	0	0	0

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Db	301	TGCCGCTACAAAAGGTAAACCTTTTATATTTTATACATTAACCTTCAGCCAGCTATTGA	360
QY	361	TATAATATAAACATTTTCAACAATACATAAAGTTAACTATTTTCTAATGTGCT	420
Db	361	TATAATATAAACATTTTCAACAATACATAAAGTTAACTATTTTCTAATGTGCT	420
QY	421	AGTTCTTTCCCTGCTTAATGAAAAGCTT	448
Db	421	AGTTCTTTCCCTGCTTAATGAAAAGCTT	448

RESULT 2	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL
BD128571	BD128571	Eosinophil eotaxin receptor.	BD128571	BD128571.1	GI:23223516	JP 2002503950-A/3.	unidentified unidentified unclassified.	1 (bases 1 to 448)	Daugherty, B.L., Demartino, J.A., Springer, M.S. and Siciliano, S.J.	Eosinophil eotaxin receptor	Patent: JP 2002503950-A 3 05-FEB-2002;

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COMMENT
OS Unidentified
PN JP 2002503950-A/3
PD 05-FEB-2002
PF 24-APR-1997 JP 1997538970
PR 26-APR-1996 US 08/640991,26-APR-1996 US 60/016158 PR
17-JAN-1997 GB 9700894.0
PI BRUCE L DAUGHERTY,JULIE A DEMARTINO,MARTIN S SPRINGER PI
PC SALVATORE J SICILIANO
PC C07K14/705,C07K14/715,C12N15/12
CC Strandedness: Single;
CC Topology: Linear;
CC Bosinophil eotaxin receptor
FH Key location/Qualifiers
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FT /organism='Unidentified'.

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QY	61	AAGCCTTCCACA CACTCACCTCTTAAAAACAGTCCCTTCAAACCTTCAGTGCACA CACTGAAGCTC	120
Db	61	AAGCCTTCCACA CACTCACCTCTTAAAAACAGTCCCTTCAAACCTTCAGTGCACA CACTGAAGCTC	120
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QY	181	ACCACAGGCCAGGGGCTGGGCAAGCTATCATCAACCCCTAAAAAGCAGAGCTTTGGCT	240
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		448 bp	DNA	linear	PAT 20-SEP-2000		

REFERENCE
AUTHORS
TITLE
JOURNAL
1 Daugherty, B.L., Demartino, J.A., Siciliano, S.J. and Springer, M.S.
Eosinophil eotaxin receptor
Patent: EP 1012190-A 4 28-JUN-2000;
MERCK & CO INC (US)

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Best local Similarity	100.0%;	Pred. No. 2.7e-83;	length 448;
Matches 448; Conservative	0;	Mismatches	0;
		Indels	0;
		Gaps	0;

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Dd	1	TAGGTGAGATGCAGAAAATTGGCTTAAAGAGGAACCAAGGAGATGAAGCAAACAATT	60	
OY		61	AAGCCTTCACACTCACCTCTAAAAAGTCTTCAAACCTCCAGTGCAACTGAAGCTC	120
Dd		61	AAGCCTTCACACTCACCTCTAAAAAGTCTTCAAACCTCCAGTGCAACTGAAGCTC	120
OY		121	TTGAAAGCACTGAAATATACACACAGCAGTAGCAGTAGATGCATGACCCTAAGGTCATT	180
Dd		121	TTGAAAGCACTGAAATATACACACAGCAGTAGCAGTAGATGCATGACCCTAAGGTCATT	180
OY		181	ACCACAGGCCAGGGGCTGGGCGAGCGTA CT CAT CAACCTTAAAAAGCAGAGCTTGGCT	240
Dd		181	ACCACAGGCCAGGGGCTGGGCGAGCGTA CT CAT CAACCTTAAAAAGCAGAGCTTGGCT	240
OY		241	TCTCTCTTAAATGAGTTACCTACATTTTAAATGCACTGAATGTTAGATAGTTACTATA	300
Dd		241	TCTCTCTTAAATGAGTTACCTACATTTTAAATGCACTGAATGTTAGATAGTTACTATA	300
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Dd		301	TGCCGCTACAAAAAGGTAAACTTTTATATTTTATACATTAACTTCAGCCAGCTATTGA	360
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Dd		361	TATAAATTAACAATTTTCACACAAATACAAATAAGTTAACTATTTTCTAATGTGCT	420
OY		421	AGTCTTCCCTGCTTAATGAAAAGCTT	448

Db 421 AGTTCCTTCCCTGCTTAATGAAAAGCTT 448

RESULT 4
AR380414

LOCUS AR380414 1717 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 959 from patent US 6607879.
ACCESSION AR380414
VERSION AR380414.1 GI:40088048
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 1717)
AUTHORS Cocks,B.G., Stuart,S.G. and Selthamer,J.J.
TITLE Compositions for the detection of blood cell and immunological response gene expression
JOURNAL Patent: US 6607879-A 959 19-AUG-2003;
Incyte Corporation; Palo Alto, CA
LOCATION/Qualifiers

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QY 181 ACCACAGGCCAGGGGCTGGGACGCTACTCATCATCAACCTTAAAGCAGAGCTTGGCT 240
DB 1450 ACCACAGGCCAGGGGCTGGGACGCTACTCATCATCAACCTTAAAGCAGAGCTTGGCT 1509

QY 241 TCTCTCTTAAATGAGTTACCTACATTTTAATGCACCTGAATGTAGATAGTACTATA 300
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RESULT 5
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LOCUS AX334894 1717 bp DNA linear PAT 09-JAN-2002
DEFINITION Sequence 5403 from Patent W00194629.
ACCESSION AX334894
VERSION AX334894.1 GI:18125613
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

REFERENCE 1 Homnidae; Homo.
AUTHORS Young,P.B., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,
Horrigan,S., Soppet,D.R. and Weaver,Z.
TITLE Cancer gene determination and therapeutic screening using signature gene sets
JOURNAL Patent: WO 0194629-A 5403 13-DEC-2001;
Avalon Pharmaceuticals (US)
LOCATION/Qualifiers

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RESULT 6
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DEFINITION Human eosinophil eotaxin receptor (CMTBR3) gene, complete cds.
ACCESSION U51241
VERSION U51241.1 GI:1480480
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1717)
AUTHORS Daugherty,B.L., Siciliano,S.J., Demartino,J.A., Malkowitz,L.,
Strocina,A. and Springer,M.S.
TITLE Cloning, expression, and characterization of the human eosinophil eotaxin receptor
JOURNAL J. Exp. Med. 183 (5), 2349-2354 (1996)
PUBMED 8642344
REFERENCE 2 (bases 1 to 1717)
AUTHORS Daugherty,B.L.

TITLE Direct Submission
JOURNAL Submitted (13-MAR-1996) Bruce L. Daugherty, Inflammation Research,
Merck Research Laboratories, R80W-107, P.O. Box 2000, Rahway, NJ
07065, USA

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QY 361 TATAAATAAAACATTTTCACACAAATACATAAGTTAACTATTATTCTAATGTGCT 420
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AR584940 1915 bp mRNA linear PAT 15-DEC-2004
LOCUS AR584940
DEFINITION Sequence 3 from patent US 6797811.
ACCESSION AR584940
VERSION AR584940.1 GI:56627916
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 1915)
AUTHORS Gray,P.W., Schweickart,V.L. and Raport,C.J.
TITLE Antibodies to chemokine receptor 88C
JOURNAL Patent: US 6797811-A 3 28-SEP-2004;
Icos Corporation; Bocheil, WA

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QY 121 TTGAAGACACTGAATATATACACAGCAGTAGAGTAGATGCACTGTAACCTAAGGTCAAT 180
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Db 1667 TCTCTCTTAAATGAGTTACCTACATTTTAATGACACCTGAATGTTAGATAGTACTATA 1726

QY 301 TGCCGCTACAAAAGGTAAACCTTTTATATTTTATACATTAACTTCAGCCAGCTATTGA 360
Db 1727 TGCCGCTACAAAAGGTAAACCTTTTATATTTTATACATTAACTTCAGCCAGCTATTGA 1786

QY 361 TATAAATAAAACATTTTCACACAAATACATAAGTTAACTATTATTCTAATGTGCT 420
Db 1787 TATAAATAAAACATTTTCACACAAATACATAAGTTAACTATTATTCTAATGTGCT 1846

QY 421 AGTTCTTCCCTGCTTAATGAAGCTT 448
Db 1847 AGTTCTTCCCTGCTTAATGAAGCTT 1874

RESULT 8
BD006761 1915 bp DNA linear PAT 31-JAN-2002
LOCUS BD006761
DEFINITION Chemokine receptors 88-2B [CCR-3] and 88C and antibodies thereof.
ACCESSION BD006761
VERSION BD006761.1 GI:18635132
KEYWORDS JP 2001029089-A/2.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 1915)
AUTHORS Gary,P.W., Sheicart,V.L. and Raport,C.J.
TITLE Chemokine receptors 88-2B [CCR-3] and 88C and antibodies thereof
JOURNAL Patent: JP 2001029089-A 2 06-FEB-2001;
ICOS CORP
COMMENT OS unidentified
PN JP 2001029089-A/2
PD 06-FEB-2001
PF 16-MAY-2000 JP 2000143832
PR 20-DEC-1995 US 08/575967, 07-JUN-1996 US 08/661393 PI
PATRICK W GARY, VICKI L SHEICART, CARROLL J RAYPORT PC
C12N15/09, C07K14/715, C07K16/24, C12N1/15, C12N1/19, C12N1/21, PC
C12N5/10,
PC C12N5/10, C12N15/02, C12P21/02, C12P21/08, C12Q1/68, G01N33/15, PC

GOIN33/50,
PC
G01N33/53, G01N33/566//A61K39/395, A61K39/395, A61K45/00, A61P7/02, PC
A61P17/06,
PC A61P19/02, A61P29/00, A61P31/12, (C12P21/02, C12R1:91), C12N15/00,
PC C12N5/00, C12N15/00
CC C12N5/00, C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT CDS 362..1426.
Location/Qualifiers
1..1915
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN

Query Match 100.0%; Score 448; DB 6; Length 1915;
Best Local Similarity 100.0%; Pred. No. 2.1e-83;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAGGTGAGATGAGAAAATTGCTTAAAGAGAGAGACCAAGAGATGAAGCAACACATT 60
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DB 1427 TAGGTGAGATGAGAAAATTGCTTAAAGAGAGAGACCAAGAGATGAAGCAACACATT 1486

QY 61 AAGCTTCCACACTCACCCTTAAACAGTCTTCAACTTCCAGTGCAACACTGAAGCTC 120
|||||
DB 1487 AAGCTTCCACACTCACCCTTAAACAGTCTTCAACTTCCAGTGCAACACTGAAGCTC 1546

QY 121 TTGAAGACACTGAAATATACACACAGCAGTAGCAGTAGCATGTACCCTAAGGTCAAT 180
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DB 1547 TTGAAGACACTGAAATATACACACAGCAGTAGCAGTAGCATGTACCCTAAGGTCAAT 1606

QY 181 ACCACAGGCCAGGGGCTGGGACGCTACTCATCAACCTTAAAGAGAGAGAGCTTGGCT 240
|||||
DB 1607 ACCACAGGCCAGGGGCTGGGACGCTACTCATCAACCTTAAAGAGAGAGAGCTTGGCT 1666

QY 241 TCTCTCTTAAATGAGTTACCTACATTTTAATGACCTGAATGTAGATAGTACTATA 300
|||||
DB 1667 TCTCTCTTAAATGAGTTACCTACATTTTAATGACCTGAATGTAGATAGTACTATA 1726

QY 301 TGGCGCTACAAAAGGTAAACCTTTTATATTTTATACATTAACCTCAGCCAGCTATTGA 360
|||||
DB 1727 TGGCGCTACAAAAGGTAAACCTTTTATATTTTATACATTAACCTCAGCCAGCTATTGA 1786

QY 361 TATTAATTAACAATTTCACACAATCAATTAAGTTAATTTTATTTCTAATGCGCT 420
|||||
DB 1787 TATTAATTAACAATTTCACACAATCAATTAAGTTAATTTTATTTCTAATGCGCT 1846

QY 421 AGTTCTTTCCCTGCTTAATGAAAAGCTT 448
|||||
DB 1847 AGTTCTTTCCCTGCTTAATGAAAAGCTT 1874

RESULT 9
BD017703 1915 bp DNA linear PAT 27-AUG-2002
LOCUS Chemokine receptors 88-2B [CKR-3] and 88C, and antibodies thereof.
ACCESSION BD017703
VERSION BD017703.1 GI:22558879
KEYWORDS JP 2001264324-A/2.
SOURCE unidentified
ORGANISM unidentified
unclassified.

REFERENCE 1 (bases 1 to 1915)
AUTHORS Gary, P.W., Schweickart, V.L. and Raport, C.J.
TITLE Chemokine receptors 88-2B [CKR-3] and 88C, and antibodies thereof
JOURNAL Patent: JP 2001264324-A 2 26-SEP-2001;
ICOS CORP
COMMENT OS Unidentified
PN JP 2001264324-A/2
PD 26-SEP-2001

PF 28-DEC-2000 JP 2000401708
PR 20-DEC-1995 US 08/575967, 07-JUN-1996 US 08/661393 PI
PATRICK W GARY, VICKI L SCHWEICKART, CARROLL J RAPORT PC
G01N33/50, A61K38/00, A61K45/00, A61P31/12, A61P31/18, C12Q1/02, PC
C12Q1/70,
PC G01N33/15, G01N33/566, G01N33/569//C07K14/705, C07K16/28, C12N15/
PC 09, C12P21/02,
PC C12P21/08, (C12Q1/02, C12R1:91), (C12Q1/70, C12R1:93), (C12P21/02,
PC C12R1:91),
PC A61K37/02, C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
CC /= '88-2B polynucleotide and amino acid sequence' FH Key
FT CDS 362..1426.
Location/Qualifiers
1..1915
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN

Query Match 100.0%; Score 448; DB 6; Length 1915;
Best Local Similarity 100.0%; Pred. No. 2.1e-83;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAGGTGAGATGAGAAAATTGCTTAAAGAGAGAGACCAAGAGATGAAGCAACACATT 60
|||||
DB 1427 TAGGTGAGATGAGAAAATTGCTTAAAGAGAGAGACCAAGAGATGAAGCAACACATT 1486

QY 61 AAGCTTCCACACTCACCCTTAAACAGTCTTCAACTTCCAGTGCAACACTGAAGCTC 120
|||||
DB 1487 AAGCTTCCACACTCACCCTTAAACAGTCTTCAACTTCCAGTGCAACACTGAAGCTC 1546

QY 121 TTGAAGACACTGAAATATACACACAGCAGTAGCAGTAGCATGTACCCTAAGGTCAAT 180
|||||
DB 1547 TTGAAGACACTGAAATATACACACAGCAGTAGCAGTAGCATGTACCCTAAGGTCAAT 1606

QY 181 ACCACAGGCCAGGGGCTGGGACGCTACTCATCAACCTTAAAGAGAGAGAGCTTGGCT 240
|||||
DB 1607 ACCACAGGCCAGGGGCTGGGACGCTACTCATCAACCTTAAAGAGAGAGAGCTTGGCT 1666

QY 241 TCTCTCTTAAATGAGTTACCTACATTTTAATGACCTGAATGTAGATAGTACTATA 300
|||||
DB 1667 TCTCTCTTAAATGAGTTACCTACATTTTAATGACCTGAATGTAGATAGTACTATA 1726

QY 301 TGGCGCTACAAAAGGTAAACCTTTTATATTTTATACATTAACCTCAGCCAGCTATTGA 360
|||||
DB 1727 TGGCGCTACAAAAGGTAAACCTTTTATATTTTATACATTAACCTCAGCCAGCTATTGA 1786

QY 361 TATTAATTAACAATTTCACACAATCAATTAAGTTAATTTTATTTCTAATGCGCT 420
|||||
DB 1787 TATTAATTAACAATTTCACACAATCAATTAAGTTAATTTTATTTCTAATGCGCT 1846

QY 421 AGTTCTTTCCCTGCTTAATGAAAAGCTT 448
|||||
DB 1847 AGTTCTTTCCCTGCTTAATGAAAAGCTT 1874

RESULT 10
AX705064 5791 bp DNA linear PAT 04-APR-2003
LOCUS Sequence 5 from Patent WO03014153.
ACCESSION AX705064
VERSION AX705064.1 GI:29561706
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE 1
AUTHORS Renzi, P., Zemzoui, K. and Lamkhioned, B.

TITLE Cellular virus receptors and methods of use
JOURNAL Patent: WO 03014153-A 5 20-FEB-2003;
Topigen Pharmaceutical Inc (CA)
FEATURES Location/Qualifiers
source 1..5791
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
4015..5082
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FTVGLGNVVVMILIKYRLIMTNIYLNLAISDLFLVTLPEWHYRGHNWVG
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AVLALPEFIFETEBELFEETLCSALYPEDTVYSWRHFHTLRMTIFCLVPLVMAIC
YTGIIKTLRCPSKKYKAIRLIFVIMAVFIFWTPYNVAILLSSYQSLIFGNDERS
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ORIGIN
Query Match 100.0%; Score 448; DB 6; Length 5791;
Best Local Similarity 100.0%; Pred. No. 1.7e-83;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TAGGTCAGATGCAGAAATTGCCTAAAGAGGAGCAAGAGATGAAGCAAAACACTT 60
Db 5080 TAGGTCAGATGCAGAAATTGCCTAAAGAGGAGCAAGAGATGAAGCAAAACACTT 5139
QY 61 AAGCCTTCACACTCACCCTCTAAACAGTCCCTCAAACTTCAGTGCAACACTGAAAGCTC 120
Db 5140 AAGCCTTCACACTCACCCTCTAAACAGTCCCTCAAACTTCAGTGCAACACTGAAAGCTC 5199
QY 121 TTGAAGACACTGAAATATACACAGCAGTAGCAGTAGATGATGATGCCCTAAGGTCAAT 180
Db 5200 TTGAAGACACTGAAATATACACAGCAGTAGCAGTAGATGATGATGCCCTAAGGTCAAT 5259
QY 181 ACCACAGGCCAGGGGCTGGGCGAGCGTACTCATCATCAACCTTAAAGAGAGAGCTTGGCT 240
Db 5260 ACCACAGGCCAGGGGCTGGGCGAGCGTACTCATCATCAACCTTAAAGAGAGAGCTTGGCT 5319
QY 241 TCTCTCTCTAAATGAGTTACCTACATTTTAATGCAACCTGAATGTTAGATGTTACTATA 300
Db 5320 TCTCTCTCTAAATGAGTTACCTACATTTTAATGCAACCTGAATGTTAGATGTTACTATA 5379
QY 301 TGGCGCTACAATAAGGTAAACCTTTTATATTTTATACATTAACCTTCAGCCAGCTATTGA 360
Db 5380 TGGCGCTACAATAAGGTAAACCTTTTATATTTTATACATTAACCTTCAGCCAGCTATTGA 5439
QY 361 TATAAATAAAACATTTTACACACATAAATAAGTTAACTATTATTCTAATGTGCTT 420
Db 5440 TATAAATAAAACATTTTACACACATAAATAAGTTAACTATTATTCTAATGTGCTT 5499
QY 421 AGTTCTTTCCCTGCTTAATGAAAGCTT 448
Db 5500 AGTTCTTTCCCTGCTTAATGAAAGCTT 5527
RESULT 11
AF247361 5791 bp DNA linear PRI 26-JUN-2002
LOCUS Homo sapiens CC chemokine receptor 3 (CCR3) gene, complete cds.
ACCESSION AF247361
VERSION AF247361.1 GI:19110542
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 5791)
Vijh,S., Dayhoff,D.E., Wang,C.E., Imam,Z., Ehrenberg,P.K. and

TITLE Michael,N.L.
JOURNAL Transcription Regulation of Human Chemokine Receptor CCR3: Evidence
PUBMED for a Rare TATA-less Promoter Structure Conserved between
12079287 Drosophila and Humans
Genomics 80 (1), 86-95 (2002)
REFERENCE 2 (bases 1 to 5791)
AUTHORS Vijh,S., Dayhoff,D.E., Wang,C.E., Ehrenberg,P.K. and Michael,N.L.
TITLE Direct Submission
JOURNAL Submitted (21-MAR-2000) Dept. of Mol. Diag. and Pathogenesis, U.S.
Military HIV Research Program, 1600 R. Gude Drive, Rockville, MD
20850, USA
FEATURES Location/Qualifiers
source 1..5791
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="3"
/map="3p21; between CCR1 and CCR5"
/clone="11A5, frag B"
/cell_type="peripheral blood mononuclear cell1"
<1..5562
/gene="CCR3"
/note="CCR3; G-protein coupled seven transmembrane
spanning receptor; principle cell-surface receptor for
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CD4/Th2 and CD8 lymphocytes, monocytes, microglia, and
dendritic cells"
/codon_start=1
/product="CC chemokine receptor 3"
/protein_id="AAL85154.1"
/db_xref="GI:19110543"
/translation="MTSLDVTVEFTGTSYDDVGLCEKADTRALMAQFVPLYSLV
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AVLALPEFIFETEBELFEETLCSALYPEDTVYSWRHFHTLRMTIFCLVPLVMAIC
YTGIIKTLRCPSKKYKAIRLIFVIMAVFIFWTPYNVAILLSSYQSLIFGNDERS
KHLDLVMLVTEVLAYSHCMMNPVIYAFVGERFRKYLRFHFRHLMHLGRYIPFLPSE
KLERTSSVSPSTAEPLSIVF"
ORIGIN
Query Match 100.0%; Score 448; DB 8; Length 5791;
Best Local Similarity 100.0%; Pred. No. 1.7e-83;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TAGGTCAGATGCAGAAATTGCCTAAAGAGGAGCAAGAGATGAAGCAAAACACTT 60
Db 5080 TAGGTCAGATGCAGAAATTGCCTAAAGAGGAGCAAGAGATGAAGCAAAACACTT 5139
QY 61 AAGCCTTCACACTCACCCTCTAAACAGTCCCTCAAACTTCAGTGCAACACTGAAAGCTC 120
Db 5140 AAGCCTTCACACTCACCCTCTAAACAGTCCCTCAAACTTCAGTGCAACACTGAAAGCTC 5199
QY 121 TTGAAGACACTGAAATATACACAGCAGTAGCAGTAGATGATGATGCCCTAAGGTCAAT 180
Db 5200 TTGAAGACACTGAAATATACACAGCAGTAGCAGTAGATGATGATGCCCTAAGGTCAAT 5259
QY 181 ACCACAGGCCAGGGGCTGGGCGAGCGTACTCATCATCAACCTTAAAGAGAGAGCTTGGCT 240
Db 5260 ACCACAGGCCAGGGGCTGGGCGAGCGTACTCATCATCAACCTTAAAGAGAGAGCTTGGCT 5319

QY	241	TCTCTCTAAAGTACCTACATTTTAATGACCTGAATGTTAGATAGTTACTATA	300
Db	5320	TCTCTCTAAAGTACCTACATTTTAATGACCTGAATGTTAGATAGTTACTATA	5379
QY	301	TGCCGCTACAAAAAGTTAACTTTTATATTTTATACATTAACCTCAGCCAGCTATTGA	360
Db	5380	TGCCGCTACAAAAAGTTAACTTTTATATTTTATACATTAACCTCAGCCAGCTATTGA	5439
QY	361	TATAATAAACAATTTTCACACATACATAAGTTAAGTTATTTTCTAATGTGCT	420
Db	5440	TATAATAAACAATTTTCACACATACATAAGTTAAGTTATTTTCTAATGTGCT	5499
QY	421	AGTCTTTCCCTGCTTAATGAAAAAGCTT	448
Db	5500	AGTCTTTCCCTGCTTAATGAAAAAGCTT	5527
RESULT 12			
LOCUS	AC138069	177334 bp	DNA linear PRI 19-FEB-2003
DEFINITION	Homo sapiens chromosome 3 clone RP13-54612, complete sequence.		
ACCESSION	AC138069		
VERSION	AC138069.3	GI:28416170	
KEYWORDS	HTG.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;		
	Hominidae; Homo.		
REFERENCE	1 (bases 1 to 177334)		
AUTHORS	Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z., Saenphimmachak, C., Buckley, D., Kibukawa, M., Raymond, C. and Haugen, E.D.		
TITLE	Direct Submission		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 177334)		
AUTHORS	Kaul, R.K., Olson, M.V., Raymond, C. and Haugen, E.D.		
TITLE	Direct Submission		
JOURNAL	Submitted (12-DEC-2002) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA		
REFERENCE	3 (bases 1 to 177334)		
AUTHORS	Kaul, R.K., Olson, M.V., Raymond, C. and Haugen, E.D.		
TITLE	Direct Submission		
JOURNAL	Submitted (10-JAN-2003) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA		
REFERENCE	4 (bases 1 to 177334)		
AUTHORS	Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z., Saenphimmachak, C., Buckley, D., Kibukawa, M., Raymond, C. and Haugen, E.D.		
TITLE	Direct Submission		
JOURNAL	Submitted (19-FEB-2003) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA		
COMMENT	On Feb 19, 2003 this sequence version replaced gi:27573398.		
TITLE	Genome Center		
JOURNAL	Center: University of Washington Genome Center		
	Center Code: UWGC		
	Web site: http://www.genome.washington.edu		
	Contact: uwgchgs@u.washington.edu		
	Project Information		
	Center project name: chr-3		
	Center clone name: RP13-54612 (bc0820)		
	Summary Statistics		
	Sequencing vector: plasmid; 100% of reads		
	Chemistry: Dye-terminator Big Dye; 100% of reads		
	Assembly program: Phrap; version 0.990319		
	Consensus quality: 177210 bases at least Q40		
	Consensus quality: 177313 bases at least Q30		
	Consensus quality: 177334 bases at least Q20		
	Insert size: 177334; sum-of-contigs		
	Quality coverage: 9.3x in Q20 bases; sum-of-contigs		
	Overlapping Sequences:		
	5': RP11-793B15 (UWGC:bc0564) AC104439, 95469-bp overlap		

3': U95626, 42710-bp overlap

Sequence Quality Assessment:
This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality ≥ 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

Sequence Validation:

This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below.

The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

HindIII EcoRI BglII

SeqDerMap	FngrPrnt	SeqDerMap	FngrPrnt	SeqDerMap	FngrPrnt
1239	1199	11125	10952	6306	6319
449	<800	2290	2310	2067	2071
510	<800	560	<800	3913	3756
6511	6363	54	<800	2169	2210
5296	5509	1159	1158	910	910
10424	10027	4052	4034	875	883
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1196	1199	8334	8273	4502	4523
1397	1392	12882	12573	1967	1945
2597	2624	448	<800	2864	2871
1688	1674	12737	12573	4724	4738
3800	3818	10300	10103	4773	4738
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1074	1055	4052	4034	336	<800
7303	7718	1392	1386	79	<800
959	959	4253	4286	4736	4738
551	<800	2791	2834	1889	1945
1074	1055	2647	2682	3696	3756

5688	5759	3423	3409	1569	1539
5183	5363	73	<800	8078	8038
3100	3093	499	<800	1365	1325
921	959	723	<800	289	<800
4350	4244	2763	2834	11047	10790
4931	4857	6594	6656	8848	8963
3907	3818	4503	4468	1914	1945
8001	7718	5154	5136	1336	1325
3804	3818	4730	4713	11485	11341
2355	2376	13628	13324	974	975
862	868	166	<800	2448	2501
1711	1674	9554	9494	373	<800
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1174	1155	520	<800	1707	1631
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221	<800	154	<800	178	<800
1002	1055	5077	5136	2905	2871
201	<800	2156	2190	2500	2501
6717	6864	1075	1089	389	<800
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2737	2749	2752	2834	685	<800
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5801	5759	1547	1503	2152	2210
1512	1497	5163	5136	431	<800
1398	1392	8679	8719	237	<800
8413	8333	2033	2035	3380	3411
6621	6614	886	892	5694	5744
645	<800			3255	3265
1026	1055			183	<800
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				10701	10790
				1321	1325

Query Match 100.0%; Score 448, DB 8; Length 177334;
Best Local Similarity 100.0%; Pred. No. 9, 8e-84;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TAGGTCAGATGCAGAAAATTGCTTAAAGAGGAAGCAAGAGATGAAGCAACATTT 60
Db 89456 TAGGTCAGATGCAGAAAATTGCTTAAAGAGGAAGCAAGAGATGAAGCAACATTT 89515
Qy 61 AAGCTTCCACACTCAGCTCTAAAACAGTCTTCAAACCTCCAGTGAACACTGAAGCTC 120
Db 89516 AAGCTTCCACACTCAGCTCTAAAACAGTCTTCAAACCTCCAGTGAACACTGAAGCTC 89575
Qy 121 TTGAAGACACTGAAATATACACACAGCAGTAGCAGTAGATGCATGTACCTAAGTCATT 180
Db 89576 TTGAAGACACTGAAATATACACACAGCAGTAGCAGTAGATGCATGTACCTAAGTCATT 89635
Qy 181 ACCACAGGCCAGGGGCTGGGCAAGCTACTCATCTCAACCCCTAAAAAGCAGAGCTTGCT 240
Db 89636 ACCACAGGCCAGGGGCTGGGCAAGCTACTCATCTCAACCCCTAAAAAGCAGAGCTTGCT 89695
Qy 241 TCTCTCTTAAATAGTTACCTACATTTAATGACCTGAATGTTAGATAGTTACTATA 300
Db 89696 TCTCTCTTAAATAGTTACCTACATTTAATGACCTGAATGTTAGATAGTTACTATA 89755
Qy 301 TGCCGCTACAAAAAGGTAATCTTTTATATTTTATACATTAACCTCAGCCAGCTATTGA 360
Db 89756 TGCCGCTACAAAAAGGTAATCTTTTATATTTTATACATTAACCTCAGCCAGCTATTGA 89815
Qy 361 TATTAATAAATACATTTTGACACAATACATTAAGTTAATTTTCTAATGTCCT 420
Db 89816 TATTAATAAATACATTTTGACACAATACATTAAGTTAATTTTCTAATGTCCT 89875
Qy 421 AGTTCTTTCCTGCTTAATGAAGCTT 448
Db 89876 AGTTCTTTCCTGCTTAATGAAGCTT 89903

RESULT 13
AC104439 197279 bp DNA linear PRI 20-JUN-2002
LOCUS Homo sapiens chromosome 3 clone RP11-793E15, complete sequence.
DEFINITION AC104439 AC024739
ACCESSION AC104439.2 GI:21490240
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 197279)
Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,
Saenphimmachak,C., Phelps,K.A., Buckley,D., Kibukawa,M., Raymond,C.
and Haugen,E.D.
Direct Submission
TITL Direct Submission
JOURN Unpublished
AUTHORS Kaul,R.K., Olson,M.V., Raymond,C. and Haugen,E.D.
TITL Direct Submission
JOURN Submitted (11-DEC-2001) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
REFERENCE 3 (bases 1 to 197279)
Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,
Saenphimmachak,C., Phelps,K.A., Buckley,D., Kibukawa,M., Raymond,C.
and Haugen,E.D.
Direct Submission
TITL Direct Submission
JOURN Submitted (20-JUN-2002) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
COMMENT On Jun 20, 2002 this sequence version replaced gi:17488621.
----- Genome Center
Center: University of Washington Genome Center
Center Code: UWGC
Web site: http://www.genome.washington.edu

Contact: uwgchtgs@u.washington.edu
Drafting Center: WUGSC
----- Project Information -----
Center project name: chr-3
Center clone name: RP11-793B15 (bc0564)
----- Summary Statistics -----
Sequencing vector: unknown; 52% of reads
Sequencing vector: plasmid; L08752; 48% of reads
Chemistry: Dye-terminator ET; 94% of reads
Chemistry: Dye-terminator Big Dye; 6% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 197168 bases at least Q40
Consensus quality: 197255 bases at least Q30
Consensus quality: 197275 bases at least Q20
Insert size: 197279; sum-of-contigs
Quality coverage: 8.2x in Q20 bases; sum-of-contigs

Overlapping Sequences:
5': RP11-91B8 (UWGC:bc0216) AC026349
3': CTD-2563A18 (UWGC:bc0730)

Sequence Quality Assessment:
This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted:
all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

Sequence Validation:
This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below.
The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

HindIII		BglII		EcoRI	
SeqDerMap	FngPrnt	SeqDerMap	FngPrnt	SeqDerMap	FngPrnt
-----	-----	-----	-----	-----	-----
2687	2617	8949	8586	8696	8661
-----	-----	-----	-----	-----	-----
6382	6410	2067	2160	6	<800
-----	-----	-----	-----	-----	-----
512	<800	7846	7940	2742	2803
-----	-----	-----	-----	-----	-----
449	<800	3734	3895	5376	5324
-----	-----	-----	-----	-----	-----
2602	2763	1334	1301	1493	1478
-----	-----	-----	-----	-----	-----
2590	2617	2287	2309	823	835
-----	-----	-----	-----	-----	-----
8313	8291	1814	1918	1962	2002
-----	-----	-----	-----	-----	-----
1711	1683	691	<800	2900	2954
-----	-----	-----	-----	-----	-----
9821	9472	5477	5348	1484	1478

-----	516	<800	305	<800	1005	995
-----	8587	8291	25245	25541	1181	1171
-----	7446	7581	3988	4121	18560	19002
-----	2088	2075	1633	1598	3603	3579
-----	2509	2617	631	<800	4943	5076
-----	3519	3501	90	<800	3239	3241
-----	26	<800	402	<800	953	995
-----	925	933	3350	3490	1621	1615
-----	98	<800	4577	4515	6827	6900
-----	6409	6410	1229	1183	79	<800
-----	1383	1376	4221	4331	16418	16263
-----	16048	15829	3980	4121	3361	3241
-----	1876	1877	2548	2497	872	881
-----	4169	4068	674	<800	4220	4193
-----	1674	1683	2332	2309	2848	2803
-----	52	<800	11445	11045	2283	2318
-----	5227	5082	5692	5632	3211	3241
-----	15464	15829	1385	1414	4615	4632
-----	14333	14296	608	<800	6823	6900
-----	1026	1026	3930	3895	886	881
-----	645	<800	1465	1414	2032	2002
-----	6621	6410	2382	2497	8680	8661
-----	8413	8291	747	<800	5163	5076
-----	1401	1376	1951	2012	1547	1478
-----	1512	1471	642	<800	7058	6900
-----	5801	5644	21060	21003	1647	1615
-----	3256	3278	3700	3666	2753	2803
-----	3448	3501	1321	1301	162	<800
-----	2738	2763	10705	10502	1078	1093
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-----	6715	6823	183	<800	5077	5076
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-----	1002	1026	5693	5632	1571	1478
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-----	2854	2899	237	<800	520	<800
-----	6998	7317	431	<800	1540	1478

1174	1145	2152	2160	1479	1478
7876	8291	249	<800	1613	1615
1911	1877	2599	2778	1399	1478
3899	3847	685	<800	9553	9383
5672	5644	41	<800	166	<800
1711	1683	388	<800	13615	13115
862	854	2500	2497	4731	4632
2368	2389	2889	2778	5159	5076
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		6589	6728	6607	6900
				2766	2803

Query Match 100.0%; Score 448; DB 8; Length 197279;

Best Local Similarity 100.0%; Pred. No. 9.7e-84;

Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	TAGGTGAGATGAGAAATTTGCCTTAAGAAGAGACCAAGAGATGAAGCAACACATT	60
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QY	121	TTGAAGACACTGAATATATACACACAGAGTAGAGTAGATGCATGTACCCTAAGTCATT	180
Db	191373	TTGAAGACACTGAATATATACACACAGAGTAGAGTAGATGCATGTACCCTAAGTCATT	191432
QY	181	ACCAAGGCCAGGGGGCTGGGCAGCGTACTCATCATCAACCCCTAAGAGAGAGCTTTGCT	240
Db	191433	ACCAAGGCCAGGGGGCTGGGCAGCGTACTCATCATCAACCCCTAAGAGAGAGCTTTGCT	191492
QY	241	TCTCTCTTAATAATGAGTTACCTACATTTTAATGACACCTGAATGTTAGATTACTATA	300
Db	191493	TCTCTCTTAATAATGAGTTACCTACATTTTAATGACACCTGAATGTTAGATTACTATA	191552
QY	301	TGCCGCTACAAAAAGTAAACCTTTTATATTATATACATTAACTTCAGCCAGCTATTGA	360
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Db	191613	TATAATTAACAATTTTCACACAAATAGTAAGTTAACTATTTTCTAATGTGCTT	191672
QY	421	AGTCTTTCCCTGCTTAATGAAAAGCTT	448
Db	191673	AGTCTTTCCCTGCTTAATGAAAAGCTT	191700

RESULT 14
HSA312688 220965 bp DNA linear HTG 15-MAY-2002
LOCUS HSA312688
DEFINITION Homo sapiens chromosome 3 clone RP6-32923 map 3p21.3, ***
SEQUENCING IN PROGRESS ***, 26 ordered pieces.

ACCESSION AJ312688
VERSION AJ312688.2 GI:13559235
KEYWORDS HTG; HTGS_PHASE2.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1

AUTHORS	Kiss,H., Yang,Y., Kiss,C., Andersson,K., Klein,G., Imreh,S. and Dumanaki,J.P.
TITLE	The transcriptional map of the common eliminated region 1 (C3CER1) in 3p21.3
JOURNAL	Eur. J. Hum. Genet. 10 (1), 52-61 (2002)
PUBMED	11896456
REFERENCE	2 (bases 1 to 220965)
AUTHORS	Kiss,H.
TITLE	Direct Submission
JOURNAL	Submitted (01-APR-2001) Kiss H., Microbiology and Tumorbiology Center (MTC), Karolinska Institute, Box 280, Stockholm, S-17177, SWEDEN
COMMENT	On Apr 5, 2001 this sequence version replaced gi:13548633. The sequence is a consensus sequence of clone RP4-787c23 (1-140400 bp), clone RP6-32923 (31212-220965 bp), clone RP6-146e1 (partially, 1-6800 bp) and clone RP6-188g11 (partially, 1-108303 bp). The sequencing contigs are in order and the gaps between them are represented by 100 Ns.
	Contig 1: 1-11731 bp Contig 2: 11832-26218 bp Contig 3: 26319-28347 bp Contig 4: 28448-42160 bp Contig 5: 42261-55059 bp Contig 6: 55160-61578 bp Contig 7: 61679-97342 bp Contig 8: 97443-117655 bp Contig 9: 117756-118727 bp Contig 10: 118828-121834 bp Contig 11: 121935-127855 bp Contig 12: 127956-129383 bp Contig 13: 129484-131747 bp Contig 14: 131848-132316 bp Contig 15: 132417-134455 bp Contig 16: 134556-135527 bp Contig 17: 135628-189051 bp Contig 18: 189152-189476 bp Contig 19: 189577-191375 bp Contig 20: 191476-201473 bp Contig 21: 201574-202307 bp Contig 22: 202408-204878 bp Contig 23: 204979-213531 bp Contig 24: 213632-218109 bp Contig 25: 218210-219800 bp Contig 26: 219901-220965 bp.
	* NOTE: This is a 'working draft' sequence. It currently consists of 26 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have been provided by the submitter.
	* This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.
	1 11731: contig of 11731 bp in length
	* 11732 11831: gap of 100 bp
	* 11832 26218: contig of 14387 bp in length
	* 26219 26318: gap of 100 bp
	* 26319 28347: contig of 2029 bp in length
	* 28348 28447: gap of 100 bp
	* 28448 42160: contig of 13713 bp in length
	* 42161 42360: gap of 200 bp
	* 42361 55059: contig of 12699 bp in length
	* 55060 55159: gap of 100 bp
	* 55160 61578: contig of 6419 bp in length
	* 61579 61678: gap of 100 bp
	* 61679 97342: contig of 35664 bp in length
	* 97343 97442: gap of 100 bp
	* 97443 117655: contig of 20213 bp in length
	* 117656 117755: gap of 100 bp
	* 117756 118727: contig of 972 bp in length
	* 118728 118827: gap of 100 bp
	* 118828 121834: contig of 3007 bp in length
	* 121835 121934: gap of 100 bp
	* 121935 127855: contig of 5921 bp in length
	* 127856 127955: gap of 100 bp
	* 127956 129383: contig of 1428 bp in length
	* 129384 129483: gap of 100 bp

* 129484 131747: contig of 2264 bp in length
* 131748 131847: gap of 100 bp
* 131848 132316: contig of 469 bp in length
* 132317 132416: gap of 100 bp
* 132417 134455: contig of 2039 bp in length
* 134456 134555: gap of 100 bp
* 134556 135527: contig of 972 bp in length
* 135528 135627: gap of 100 bp
* 135628 189051: contig of 53424 bp in length
* 189052 189151: gap of 100 bp
* 189152 189476: contig of 325 bp in length
* 189477 189576: gap of 100 bp
* 191376 191375: contig of 1799 bp in length
* 191476 201473: contig of 9998 bp in length
* 201474 201573: gap of 100 bp
* 201574 202307: contig of 734 bp in length
* 202308 202407: gap of 100 bp
* 202408 204878: contig of 2471 bp in length
* 204879 204978: gap of 100 bp
* 213532 213531: contig of 8553 bp in length
* 213532 213631: gap of 100 bp
* 218110 218109: contig of 4478 bp in length
* 218210 219800: contig of 1591 bp in length
* 219801 219900: gap of 100 bp
* 219901 220965: contig of 1065 bp in length.

FEATURES

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1. 220965
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/db_xref="taxon:9606"
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ORIGIN

Query Match 100.0%; Score 448; DB 14; Length 220965;
Best Local Similarity 100.0%; Pred. No. 9.5e-84;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAGGTGAGATGCAGAAATTGCTTAAAGAGAGAGACCAAGAGATGAAGCAACACATT 60
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QY 61 AAGCTTCCACACTCACCCTCTAAACAGTCTTCAAACTTCCAGTGCAACACTGAAGCTC 120
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QY 121 TTGAAGACACTGAAATATACACAGCAGTAGCAGTAGATGCATGTACCCTAAGTCAAT 180
Db 141449 TTGAAGACACTGAAATATACACAGCAGTAGCAGTAGATGCATGTACCCTAAGTCAAT 141508
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Db 141509 ACCACAGGCCAGGGGCTGGGCGAGCGTACTCATCATCAACCTTAAAGACAGAGCTTGGCT 141568
QY 241 TCTCTCTCTAAATGAGTTACCTACATTTTAATGCACCTGAATGTTAGATAGTTACTATA 300
Db 141569 TCTCTCTCTAAATGAGTTACCTACATTTTAATGCACCTGAATGTTAGATAGTTACTATA 141628
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QY 361 TATAAATAAAACATTTTACACACATTAACAATAAGTTAACTATTATTTTCTAATGTGCTT 420
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RESULT 15
AKI23050
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

1913 bp mRNA linear PRI 30-JAN-2004
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to C-C CHEMOKINE RECEPTOR TYPE 3.
AKI23050
AKI23050.1 GI:34528507
Oligo capping; fis (full insert sequence).
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Ctenata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE
AUTHORS

1
Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R.,
Wakamatsu, A., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H.,
Sekine, M., Ohtsuka, S., Yoshikawa, Y., Matsunawa, H., Ichihara, T.,
Ishii, S., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y.,
Nagahari, K., Murakami, K., Yasuda, T., Iwayanagi, T., Wagatsuma, M.,
Shiratori, A., Sudo, H., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H.,
Sugawara, M., Takahashi, M., Kanda, K., Yokoi, T., Furuya, T.,
Kikkawa, E., Omura, Y., Abe, K., Kamihara, K., Katsuta, N., Sato, K.,
Tanikawa, M., Yamazaki, M., Ninomiya, K., Ishibashi, T., Yamashita, H.,
Murakawa, K., Fujimori, K., Tanai, H., Kimata, M., Watanabe, M.,
Hiraoaka, S., Chiba, Y., Ishida, S., Ono, Y., Takiguchi, S., Watanabe, S.,
Yosida, M., Hotuta, T., Kusano, J., Kanehori, K., Kanehori, K., Takahashi, A.,
Hara, H., Tanase, T., Nomura, Y., Togiya, S., Komai, F., Hara, R.,
Takeuchi, K., Arita, M., Imose, N., Musashino, K., Yuki, H., Oshima, A.,
Sasaki, N., Aotsuka, S., Yoshikawa, Y., Matsunawa, H., Ichihara, T.,
Shiohata, N., Sano, S., Moriya, S., Momiyama, H., Satoh, N., Takami, S.,
Terasima, Y., Suzuki, O., Nakagawa, S., Senoh, A., Mizoguchi, H.,
Goto, Y., Shimizu, F., Wakebe, H., Hishigaki, H., Watanabe, T.,
Sugiyama, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, K.,
Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M.,
Tashiro, H., Tanigami, A., Fujiwara, T., Ono, T., Yamada, K., Fujii, Y.,
Ozaki, K., Hirao, M., Ohmori, Y., Kawabata, A., Hiki, T., Kobatake, N.,
Inagaki, H., Ikema, Y., Okamoto, S., Ohtani, R., Kawakami, T.,
Noguchi, S., Itoh, T., Shigetani, K., Senba, T., Matsumura, K.,
Nakajima, Y., Mizuno, T., Morinaga, M., Sasaki, M., Togashi, T.,
Oyama, M., Hata, H., Watanabe, M., Komatsu, T., Mizushima-Sugano, J.,
Satoh, T., Shirai, Y., Takahashi, Y., Nakagawa, K., Okumura, K.,
Nagase, T., Nomura, N., Kikuchi, H., Masuo, Y., Yamashita, R.,
Nakai, K., Yada, T., Nakamura, Y., Ohara, O., Isogai, T. and Sugano, S.
Complete sequencing and characterization of 21,243 full-length
human cDNAs
Nat. Genet. 36 (1), 40-45 (2004)
14702039

JOURNAL
PUBMED
REFERENCE
AUTHORS

2
Suzuki, O., Sasaki, N., Aotsuka, S., Shoji, T., Ichihara, T.,
Shiohata, N., Matsumoto, K., Hirano, M., Sano, S., Nomura, R.,
Yoshikawa, Y., Matsumura, Y., Moriya, S., Chiba, B., Momiyama, H.,
Kotagawa, S., Kaeriyama, S., Satoh, N., Matsunawa, H., Takahashi, B.,
Kataoka, R., Kuga, N., Kuroda, A., Satoh, I., Kamata, K., Takami, S.,
Terasima, Y., Watanabe, M., Sugiyama, T., Irie, R., Otsuki, T.,
Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y.,
Kawai, H., O., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H.,
Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K.,
Wagatsuma, M., Murakawa, K., Kanehori, K., Takahashi, F.,
Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S.,
Nagahari, K., Masuo, Y., Nagai, K. and Isogai, T.
NEBO human cDNA sequencing project
Unpublished
3 (bases 1 to 1913)

JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

COMMENT

Isogai, T. and Yamamoto, J.
Direct Submission
Submitted (15-JUL-2003) Takao Isogai, FLJ Project (HRI Team); 2-6-7
Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEBO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction: Helix Research Institute (HRI) (supported by Japan

Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.

FEATURES

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1. 1913
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ORIGIN

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Best Local Similarity	100.0%;	Pred. No. 2.9e-70;		
Matches 385;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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QY	61	AAGCTTCCACACTCACCCTTAATAACAGTCTTCAAACTTCCAGTGCACACTGAAAGCTC	120	
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QY	181	ACCAAGGCCAGGGGCTGGCAGCGTACTCATCATCAACCCCTAATAAAGCAGAGCTTGGCT	240	
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Job time : 2209.58 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using SW model

Run on: January 7, 2006, 07:05:07 ; Search time 668.111 Seconds
(without alignments)
3912.475 Million cell updates/sec

Title: US-10-767-521-3

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Scoring table: IDENTITY NUC
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Searched: 4637609 seqs, 364468668 residues

Total number of hits satisfying chosen parameters: 9275218

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 7: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq2:*
- 9: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq3:*
- 10: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	344.2	9.6	1915	7	US-11-068-686-3 Sequence 3, Appli
2	319.2	8.9	2613	6	US-10-750-185-39572 Sequence 39572, A
3	319.2	8.9	2613	6	US-10-750-623-39572 Sequence 39572, A
4	211.4	5.9	187745	7	US-11-121-086-83 Sequence 83, Appl
5	209	5.8	215308	7	US-11-121-086-77 Sequence 77, Appl
6	208.2	5.8	56448	6	US-10-995-561-13369 Sequence 13369, A
7	208.2	5.8	235033	7	US-11-157-389-1 Sequence 1, Appli
8	206.8	5.8	171162	7	US-11-112-908-38 Sequence 38, Appl
9	206.4	5.8	130472	6	US-10-995-561-13312 Sequence 13312, A
10	204.4	5.7	246960	7	US-11-121-086-8 Sequence 8, Appli
11	204.2	5.7	1080000	6	US-10-928-446A-1 Sequence 1, Appli
12	204.2	5.7	1080000	6	US-10-928-446A-181 Sequence 181, App
13	204.2	5.7	1080000	6	US-10-928-446A-183 Sequence 183, App
14	204.2	5.7	1080000	6	US-10-928-446A-185 Sequence 185, App
15	204.2	5.7	1080000	6	US-10-928-446A-187 Sequence 187, App
16	204.2	5.7	1080000	6	US-10-928-446A-189 Sequence 189, App
17	204.2	5.7	1080000	6	US-10-928-446A-191 Sequence 191, App
18	204.2	5.7	1080000	6	US-10-928-446A-193 Sequence 193, App
19	204.2	5.7	1080000	6	US-10-928-446A-195 Sequence 195, App
20	204.2	5.7	1080000	6	US-10-928-446A-197 Sequence 197, App
21	204.2	5.7	1080000	6	US-10-928-446A-199 Sequence 199, App
22	204.2	5.7	1080000	6	US-10-928-446A-201 Sequence 201, App
23	203.4	5.7	165156	6	US-10-995-561-13304 Sequence 13304, A

C	24	202.6	5.6	115935	6	US-10-775-169-241	Sequence 241, App
C	25	202.6	5.6	162289	7	US-11-121-086-20	Sequence 20, Appl
C	26	202.6	5.6	387780	6	US-10-995-561-13259	Sequence 13259, A
C	27	202.2	5.6	44848	7	US-11-106-672A-42	Sequence 42, Appl
C	28	201.8	5.6	319608	7	US-11-145-703-1	Sequence 1, Appli
C	29	201.4	5.6	5982	7	US-11-034-771-1	Sequence 1, Appli
C	30	201.4	5.6	15804	6	US-10-995-561-13294	Sequence 13294, A
C	31	201.4	5.6	24446	6	US-10-995-561-13436	Sequence 13436, A
C	32	201.4	5.6	153142	7	US-11-121-086-27	Sequence 27, Appl
C	33	201.4	5.6	191684	7	US-11-121-086-2	Sequence 2, Appli
C	34	201.2	5.6	191331	7	US-11-112-908-20	Sequence 20, Appl
C	35	201.2	5.6	196200	7	US-11-121-086-9	Sequence 9, Appli
C	36	201.2	5.6	246960	7	US-11-121-086-8	Sequence 8, Appli
C	37	201	5.6	5515	6	US-10-517-605-14	Sequence 14, Appl
C	38	201	5.6	5515	7	US-11-055-309A-2	Sequence 2, Appli
C	39	201	5.6	40000	6	US-10-995-561-13513	Sequence 13513, A
C	40	201	5.6	180862	7	US-11-112-908-40	Sequence 40, Appl
C	41	200.8	5.6	98716	6	US-10-995-561-13331	Sequence 13331, A
C	42	200.8	5.6	150314	7	US-11-112-908-24	Sequence 24, Appl
C	43	200.8	5.6	159497	7	US-11-112-908-61	Sequence 61, Appl
C	44	200.8	5.6	171427	7	US-11-112-908-60	Sequence 60, Appl
C	45	200.6	5.6	237326	7	US-11-157-389-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-11-068-686-3
Sequence 3, Application US/11068686
Publication No. US20050260565A1
GENERAL INFORMATION:
APPLICANT: Gray, Patrick W.
Schweickart, Vicki L.
Raport, Carol J.
TITLE OF INVENTION: Chemokine Receptor Materials and Methods
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/068, 686
FILING DATE: 28-Feb-2005
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Noland, Greta B.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/33670
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1915 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 362..1426
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: /= "88-2B polynucleotide and amino acid

SEQUENCE	DESCRIPTION	SEQ ID NO	3
US-11-068-686-3			

Query Match	9.6%;	Score 344.2;	DB 7;	Length 1915;
Best Local Similarity	98.9%;	Pred. No. 6.6e-65;		
Matches 357; Conservative	0;	Mismatches 3;	Indels 1;	Gaps 1;

[illegible]

RESULT 2

US-10-750-185-39572/c
; Sequence 39572, Application US/10750185
; Publication No. US20050260603A1

GENERAL INFORMATION:

```

; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISER, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MMI1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39572
;
; LENGTH: 2613
;
; TYPE: DNA
;
; ORGANISM: Bovine 19866881243305
US-10-750-185-39572

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Query Match	8.9%;	Score 319.2;	DB 6;	Length 2613;
Best Local Similarity	60.0%;	Pred. No. 1.9e-59;		
Matches 1251; Conservative	0;	Mismatches 578;	Indels 255;	Gaps 33;

OY	1538	TCAATCCGTGATCATGTTGATT	TTTATAGAAATAACACATGAATTAAGA	CACACTACCCTCGAAA	1597
D6	2613	TTAACAATCATCATGTAGGATT	TTATGGAAATGACACATGAATTTAAAG--	ATGATCTTCGAAG	2556
OY	1598	CTGAGCAAACCTTAAGTAA----	TTTTTTTAAAGTTTGACCTGTTTTTAAATC	ACTCTCTTG	1653

Db	2555	TTGGAAAA	CACTTCA	GTGA	AAATTC	TTTTTT	TA	AG	TTTG	ACTT	GT	TTT	TC	AG	AT	CA	GT	CT	GT	2496		
Qy	1654	GAGAAAAA	GGAAAA	TAA	TACAA	ATTA	TA	CG	GTAA	TAC	AG	GT	CT	ACT	TA	TAC	TT	GT	1713			
Db	2495	GAG-AAA	GGAAAA	GA	AAATAT	TAA	TTA	TGA	TAG	TAG	AG	GT	CT	-----	2449							
Qy	1714	CTCCAGA	ATTAG	CAG	TTCT	GT	CTTT	CT	GT	TTA	GAT	GT	CT	GA	AG	CA	GA	CA	ACT	1773		
Db	2448	-----	-----	-----	TT	CA	CT	CT	GT	CT	TA	AA	CA	TTA	AG	GT	TA	GA	GAT	2409		
Qy	1774	CTG-TG	ATTG	TAC	GT	GT	TACT	GC	CA	AA	ATG-T	GT	AT	TTTT	TTTT	TT	CT	CA	GT	CT	1831	
Db	2408	CTCAT	GACCG	AAAA	TGC	ATA	CA	GAC	CA	AA	TGA	TGG	GT	ACT	TTT	TT	CT	CA	GT	CT	2353	
Qy	1832	TTGAT	TATG	CTA	TTAT	TGA	TAA	GAA	TG	CTGA	TGG-G	-G	AG	CA	CA	CA	CA	AA	CA	TT	1890	
Db	2352	-TGT	ATTAT	GCC	ATTG	GGA	ATTT	TTA	AAAA	GCT	GT	TA	AG	AT	CA	TAT	TA	AG	TC	AG	2294	
Qy	1891	TCAG	TCCAT	TTT	CCT	CT	CA	AA	AG	CT	GA	A	TG	TC	CA	T	TG	AT	CA	T	1950	
Db	2293	TCA	ATTCC	ATTT	TAA	CCT	CG	AA	AG	CT	GA	A	TG	TC	CA	T	TA	G	AT	GA	2234	
Qy	1951	GGAC	AGAC	CCAT	GA	AA	AG	AT	CA	CA	AG	TT	CA	CC	CA	AG	GA	CC	CTA-T	TTTT	2009	
Db	2233	GGCC	AGAG	CTAT	GA	AA	AT	AG	AT--	CA	AG	TT	CA	TC	CA	AG	AG	CT	CT	ACT	2177	
Qy	2010	TTCA	TTGA	AAT	GG	CTT	CT	AA	T	TG	T	CT	CT	TT	CA	TT	C	T	G	CT	2067	
Db	2176	TTCA	TG	TAA	AC	CA	TT	CT	CA	T	TG	CT	TT	CT	CA	CT	T	G	CT	TT	2117	
Qy	2068	AG	CTTT	TT	CT	GG	TT	CA	AA	T	G	AA	CT	CA	TA	CA	CT	CA	TT	TT	2127	
Db	2116	TT	CTTT	TT	CT	AG	TT	TAA	AT	T	GA	T	CA	T	GA	CA	CT	CT	GA	TT	2057	
Qy	2128	CA	AG	T	ACC-----	CA	T	G	T	CT	CT	CA	TT	TC	AA	T	A	G	T	A	2182	
Db	2056	CA	AT	T	GG	T	GG	CT	AC	CA	T	AT	CT	TT	T	G	A	T	A	A	1997	
Qy	2183	GG	CT	T	TC	CA	AG	GA	CG	CA	G	CTG-----	A	G	AG	CG	CT	A	G	A	2236	
Db	1996	GG	CT	T	G	T	CT	GA	T	CT	CT	CA	T	G	CA	AG	CA	GA	A	T	1937	
Qy	2237	CT	AT	TT	CT	CA	T	G	CT	T	GA	CT	AC	CC	CA	AA	CC	CA	A	T	2296	
Db	1936	CT	CT	CT	AC	AG	T	CA	TT	G	A	CC	CA	CA	CA	GA	AC	CC	CA	A	1877	
Qy	2297	AT	T	AT	TT	CT	A	T	A	GA	CA	AA	AA	CA	AT	T	C	C	G	A	2356	
Db	1876	AT	TT	TT	CT	T	AG	A--	A	G	CA	AA	GA	CA	A	T	C	T	T	G	1821	
Qy	2357	C	A	G	A	T	T	A	C	T	T	G	A	A	T	G	C	C	A	T	G	2416
Db	1830	A	A	G	C	C	T	G	C	T	T	G	A	A	T	A	C	T	G	T	A	1764
Qy	2417	C	C	T	C	T	A	G	A	A	G	A	A	G	T	C	A	G	T	G	A	2476
Db	1763	--	T	C	A	G	A	A	A	G	A	G	T	T	A	G	A	G	A--	CT	CT	1709
Qy	2477	G	T	C	T	T	C	A	T	G	A	C	T	C	T							

Qy	2717	AGTAACCTAACTAATGCTGCTTATTAATTTGTAATTAATGTAATAGTTAATTAATGCTGATTT	2776
Db	1481	ACGCTGCT-TACAATTGTTACAACAGTTAATACTACTACACACAGCTAATTATTAATTT	1423
Qy	2777	GTACATGTGTAAACAGACAAATGTGTATTTTTCACAGCTGCTGTGATTTGATTAATGC	2836
Db	1422	-----	-----
Qy	2837	CATTGGAATAAGAAATGCTGTTAAGAGACACAAAGCCAGTTCTCAAGTCCGTAGCAAA	2896
Db	1422	-----	-----
Qy	2897	TTTTCAAAAGTTAAATTTTAAAAATCACTACATTGATCTAGTACAGAGAAATGAC	2956
Db	1422	-----ATTATTAAGTTAAAAATCACTGTACTTGAATCCAGTGATGAGAGAAATTCAGC	1372
Qy	2957	ATGATAGAGACTAAAGATCTAGCCCAATTTTATATTTACTTGTAGAGATTTGAAC	3016
Db	1371	ATAGATACTGAAGATCTAGC---CTGAACTTTGAAATGCTTACTAAAGGATTTTAGAC	1315
Qy	3017	AAATTACTAAATTTCTTCAAGGTTCAATTTCCCAATTA-----ACTATAATGAATGCT	3070
Db	1314	TCCTTATTAATTTCTTGAAGTTCATTTCCCAATTACTGTATTTTAAATTTGCATTT	1255
Qy	3071	CATCATTTAGGGCCCTGAGAAAGCATTAATTACTTGTAAATTTGTAATATCATTTGTTATTA	3130
Db	1254	TTATGTTATGAGCCATGGAATGGGTAGTTATTTCTAAGGATTAATATCATTAATTA	1195
Qy	3131	TTATTTATACATATTTTGTCTTTTAAATGAGTAAGGATTTTAAAGTATATGTAAACTGTAA	3190
Db	1194	-----GCATTTGGTTTTTAAATGAT--GATTTGAAGGTCATATATATAAACATTA	1146
Qy	3191	AACATAAATGCAAAATGCCGTAAAGACAGTAGTAATTAATGATTAATATATTTGTTA	3250
Db	1145	AACATAAAA--CAAAAATTTTAAATACAGTGATAATAATATTAATTAAGATTATTTGTA	1088
Qy	3251	TCATTATCTAGCCCTGTTTTTCTCTGTGTGTATTTCTTCTTAAATGCTTACAGAAATC	3310
Db	1087	ACATTACCCCAACCTATCTCTCTGTTTTGTATTTCTTCTTCCAATATGCTTTGAG--GATC	1029
Qy	3311	TGTATCCCCCATTTCTTACCAACCACCCCACAACATTTCTGCTTCTTTTCCCATGCCG--TC	3369
Db	1028	AACATCTCCGCTCTTCACTAACATC--CACAAATGTTGTTCTTTTCCCATGATGATC	972
Qy	3370	ATGCTAATTTGAAAGCTTGAGCTCTTTCCTTCC-----TCAATCCTTCTCCTGGAC	3422
Db	971	ATGCTGACTCTCAAAACATGCGATCTTTCACCTCTAACAATTTCTCCCGCCCATGGCAT	912
Qy	3423	CTCTGATATGCTTTTGAATTCATGTTTAAAGATCCCTAGGCTGCTATCACATGTGCA	3482
Db	911	ATCTGATACACCTTTGGAATATATGCTGAAGAATGTATAGCT--ATTATTTCCGTG	854
Qy	3483	TCTTTGTTGAGTACATGAATTAATCAACTGTGTGTTTAAAGAAAGATGATTAATGCTTCA	3542
Db	853	GTTTAAAGTGAAGTGAATTAACCTGACTGTGTGGGTCTCAAGAGCGATCATCGTTAA	794
Qy	3543	TTGTGGATTGTATTTTCTTCTTCTATCACAGGAGAAATGAA	3586
Db	793	CTGTGGGGTACTTTTGCCCTTCTTCTATCACAGGAGCAAGGAA	750

RESULT 3
 US-10-750-623-39572/c
 ; Sequence 39572, Application US/10750623
 ; Publication No. US20050287531A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MMI GENOMICS, INC.
 ; APPLICANT: DENISE, Sue K.
 ; APPLICANT: KERR, Richard
 ; APPLICANT: ROSENFELD, David
 ; APPLICANT: HOLM, Tom
 ; APPLICANT: BATES, Stephen

```

; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39572
; LENGTH: 2613
; TYPE: DNA
; ORGANISM: Bovine 19866881243305
US-10-750-623-39572

Query Match      8.9%; Score 319.2; DB 6; Length 2613;
Best Local Similarity 60.0%; Pred. No. 1.9e-59;
Matches 1251; Conservative 0; Mismatches 578; Indels 255; Gaps 33;

QY      1538 TCATCCTGATCATGTGTGATTTTATAGAAATACACATGATTAAGACACTACCTCAAA 1597
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      2613 TTACACTCATCATGTAGGATTATGAAATGACACATGAATTAAG--ATGATCTTCAAG 2556

QY      1598 CTGAGCAAAACTTAAGTAA---TTTTTTAAAGTTTGACCTGTTTTAAATCACTCTTG 1653
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      2555 TTGAAAACACTTCAGTGAATTCCTTTTAAAGTTTGACCTGTTTCAGATCAGTCTGT 2496

QY      1654 GAGAAAAAGAAATAAATACAAATAATTACGCGTAATACAGGCTACTATACCTTGT 1713
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      2495 GAG-AAAAGAAAGAAATAATAATAATTAAATGATGAGTAAAGAGGCTCT----- 2449

QY      1714 CTCAGATTAGCAGTTCGTCTTTCTTTCTTTGCTTTAGATGCTGAAGTGCAAGACACT 1773
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      2448 -----TTCCACTCTTGCTTTAAACATTAAGGTTTGAAGACATACT 2409

QY      1774 CTG-TGATTGTACGTGTGTAACTGACAAATG-TGTATTTTCTCAGCTGCTAATGA 1831
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      2408 CTCATGACCGAAATGCATAACAGACCAATGATGGTACTTTTCTCAGCTGTG--- 2353

QY      1832 TTGATTATGCTATTATGAATAGAATGCTGATGG-GAGCACACACAAACATTGTTC 1890
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      2352 -TGTATTATGCCATGGGAATTTTAAAAAGCTGGTAAAGATCATATAAGTCAGTGTAC 2294

QY      1891 TCAGTCCATTTTCTCTCTCAAAAGCCTGGAAATGCCATTGATCAGTGGAGATGTACT 1950
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      2293 TCAATTCATTTTAACTCGAAAGCCTGAAATGTGTCACTGATTAGTAGATGAACCA 2234

QY      1951 GGAACAGACCCATGAAAAGAGATCAACAAGTTCCACCCCAAGGGACCCTA-TTTTCTTAAT 2009
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      2233 GGCCAGAGCTATGAAAATAGAT---CAAGTCTATCCAAAGAGCCTACTTTTCCGAT 2177

QY      2010 TTCAATTGAATGCTTCTAATGTCTCTTCAATTCCTTCACTCTGCTTCTACC--AGTTTAC 2067
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      2176 TTCATGTGAACCACTTCTCATTTGCTTCTTCACTTCTGCTTCTACCATACAGTTT 2117

QY      2068 AGCTTTTCTGTGTTCAATATGTAAGTCAATACATCTCATTTTCTCATCAACCC 2127
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      2116 TTCCTTTTCTAGTTTAAATATGATCTCATATGACTCTCTGATTTGATGCTCACCAAT 2057

QY      2128 CAAGTGACC-----CAATGCTCTCACTTTCGATATTAAGTAAAGAGGCTCTGCATTAA 2182
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      2056 CAATGGGTGGCTACATGATCTTATTTTGAGATGAATAAACGAGGCTCAGAGTTAAG 1997

QY      2183 GGCTTGTCCAAGGACGCACTG-----AGAGCGCTAGGACTGGCTCCATTTCATCT 2236
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      1996 GGCTTGTCTGAGTCTTCTCACTGGCAAGCAATGGCCAGGAACGCTCTATGTCTCTC 1937

QY      2237 CTATTTCTACTGACTTTGACTACCCAGAACCCCAACATGTGGGCTCAGTATTCATCA 2296
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      1936 CTCTCTACAGTCACTTGACACACAGAACCCCAACAGGTGCTGACTTTAGGATCCAGT 1877

QY      2297 ATTATTTATTAAGAACAAACAAATTCCTCCCGCATGGGCCCCAGTTATTAAGCATTTCT 2356
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Db	1876	ATTTCCTTAGGA--AAGCAAGAACAATCCTTGCCATCGGCTCCAAATTACT--GCATTTCT	1821
QY	2357	CAGATTACCTTGAGAAATGCCCATCGGCTGTATATTCACATCTCAACCCTTGCCCTT	2416
Db	1820	AAGCCCTGCCTTGAGAAATACTGCTGAC--GTATGTCATGACCTCACACTTGCTT-	1764
QY	2417	CCTCCTAGAAAGAGAAAGTCAGTGGATGCCCTCTGAGAACTAGTGCATGCTTAATCT	2476
Db	1763	--TCACAGAAAAAGAGAGTTAGCAGGA--CTCCTGAGAAACAGGGTAGGGTTAGCT	1709
QY	2477	GTCCCTTCATGACTCCGCTTATCTGTTTTCTATTTCTCTTTCCACCGAATCTA	2536
Db	1708	GCCTTTCATGACTACTCCCTGTCTCT--TTTCTCTCTTCTCCAGCCAGGCTG	1655
QY	2537	TAATCTCAAGAAAGCAGGCACTGGCCTTAGGGCTCCGTGCTAAGAAATATCAAGTCCA	2596
Db	1654	TAATTTCAAGAAAGCAGGCACTGACCCCTAGGGATCTGTCTAAAAAATCCAAATCTA	1595
QY	2597	GTGAGAAATCCCATTGACTGACCCCTCCTGCTTACCCTTTGTGATGAGAGCTCCAG	2656
Db	1594	AGAAAGTAGTCCCATGTGTACATGCTCAG-----CCTCTTATGAGGAGAACTCTAAG	1541
QY	2657	GGGTTTGCTTTTGCATGTTCACAGGCTTAATCTCAGCATCACAGGGCAAGAAAGAA	2716
Db	1540	GGGTCTGTGTAGGCACATGA-CTGGCTTATGTACAGATTGTCAAGAACAGAAAGGGG	1482
QY	2717	AGTAACCTAAACTAATGCTGCTTATATTTGTAATTTATTTAATAGTTAATTACTGTGATT	2776
Db	1481	ACGCTGCT-TACAATGTGTACAACAGTTAATACTACTACACAACAGTAATTATTAATTT	1423
QY	2777	GTACATGTGTACAGACAAAAATGTATTTTTTTCACAGCTGCTGTGATTGATTATGC	2836
Db	1422	-----	1423
QY	2837	CATTTGGAATAGAATGCTGTTTAAGACACACAGCCAGTTCTCAAGTCCGTAGCAA	2896
Db	1422	-----	1423
QY	2897	TTTTTCAAAAGTTAAATTTAAAAATCACTACATTGTAATCTAGTACAGAGAAATGAC	2956
Db	1422	-----ATTATTAAGTTAAAAATCACTGTACTGTAATCAGTATGAGAGAAATTCAGC	1372
QY	2957	ATGATAGAGACTAAAGATCTAGCCCAAAATTTATATTTACTGTGTAGAGATTTGAAC	3016
Db	1371	ATAGATACTGAAGATCTAGC---CTGAACCTTTGAATGCTTAAAGATTTTAGAC	1315
QY	3017	AAATTAATAATTTCTTCAAGGTTCAATTTCCCATTA-----ACTATATGAATGCT	3070
Db	1314	TCCTTATTAATTTCTTTGAGGTTCAATTTCCCATTTACTGTATTTTAAATTTGCATT	1255
QY	3071	CATCATTTATGGGCCCCGAGAGACATAATTTACTTGTATTTGTAATATCATTTGTTATTA	3130
Db	1254	TTATGTTATGAGCCATGGAATGGGTAGTTATTTCTAAGGATTAATATCACTATTTATTA	1195
QY	3131	TTATTTATACATATTTTGTCTTTAAATGAGTAAGATTTTAAAGGTATATGTAAACGTGAA	3190
Db	1194	-----GCATTGGTTTTTAAATGAT--GATTTGAAGGTCAATATATMAACCAATAA	1146
QY	3191	AACATAAAATGCAAAATGCCGTAAAGACAGTAGTAATAATTAATGATTATTTATTTGTTA	3250
Db	1145	AAACATAAAA--CAAAAATTTTAAATACAGTGATAATATTAATTAAGATTATTTGTTA	1088
QY	3251	TCATTTATCTAGCCTGTTTTTCCGTGTGTATTTCTTCCTTAAATGCTTACAGAAATC	3310
Db	1087	ACATTTAACCCAACCTATCTCTCTGTGTGTATTTCTTCCCAAAATGCTTTCAG--GATC	1029
QY	3311	TGTATCCCCCATTTCTCACCAACCAACCAACATTTCTGTCTTTTCCCATGCGCG--TC	3369
Db	1028	AACATCTCCGCTCTTCACTACCATC--CACAATGTTTGTTCCTTTCCCATGATGATC	972
QY	3370	ATGCTAACTTTGAAAGCTTCAAGCTTTTCTCTCC-----TCAATCCTTCTCTGGCAC	3422
Db	971	ATGCTGACTCTCAAAACATTTGACTTTTCACTCCTTAACATTTCTCCCGCCCATGGCAT	912

QY 3423 CTCTGATATGCCTTTGGAAATTTCATGTTAAAGAAATCCCTAAGGCTGCCTATCACAATGTGGCA 3482
| | | | | | | | | | | | | | | | |
Db 911 ATCTGATACACCCTTGGAAATATATATGCTGAAGAATGTATAGGCT - ATTATTCGGTG 854

QY 3483 TCTTGTGTAAGTACATGAATAATCAACTGGTGTGTTTTCGAGAGATGATATGCTTCA 3542
| | | | | | | | | | | | | | | | |
Db 853 GTTTTAGTGGTAAAGTAATAAAGTGACTGGTGGGTCTCAAGAGCGATCATCGTTAA 794

QY 3543 TTGTGGATTGTATTTTTCTTCTTCTATCACAGGAGAAAGTGAA 3586
| | | | | | | | | | | | | | | | |
Db 793 CTGTGGGGTTACTTTTGCCTTCTTCTATCACAGGACAAGGAA 750

```

RESULT 4
US-11-121-086-83
; Sequence 83, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 83
; LENGTH: 187745
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-83

```

[illegible]

```

; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77
; LENGTH: 215308
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-11-121-086-77

```

Query Match	5.8%	Score 209;	DB 7;	Length 215308;
Best Local Similarity	75.4%;	Pred. No. 7.3e-35;		
Matches 260; Conservative	0;	Mismatches 85;	Indels 0;	Gaps 0;

Qy	1058	TTTTAATTTTTTAA	TTTTTAATTA	TTTATTTA	TTTTTTGAGATGAGTCTGG	1117
Db	81796	TTTATTTA	TTTATTTA	TTTATTTA	TTTATTTA	TTTGAACGAGTCTCGCT
		81855				

Oy	1118 CTGTCGCCCAAGCGTGAAGTGACAGCGCGGTGATCACAGTTCACTGCAGCCTCAACCTTCTTA	1177
Db	81856 CTGTCGTCCAAGCGTGATTGACAGTGGCTTGATCTCGGCTCACCGCAACTCCGCCCCCA	81915

[illegible][illegible][illegible]

QY	1358	ACAAGCATGAGCCAAAGTCCCTGCCCATATGAGTTTTCGTCT	1402
Db	82096	ACAGGCATGAGCCCAACCATGCCCCAGCCCTTTTTTTTTTTTTTT	82140

RESULT 6

```

US-10-995-561-13369
; Sequence 13369, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13369
; LENGTH: 56448
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(56448)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1
US-10-995-561-13369

```

Query Match	5.8%;	Score 208.2;	DB 6;	Length 56448;
Best Local Similarity	77.9%;	Pred. No. 6.2e-35;		
Matches 264;	Conservative	0;	Mismatches 73;	Indels 2;
				Gaps 1;

```

QY      1047 CCATATCAGGTTTAAATTTTAAATTTTAAATTAATTAATTTATTTTGG 1106
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      33145 CAAGATAAGGTGTAAATGTACTATTTTAATTAATTTTATTTTATTTTGG 33204

```

OY	1107	ATGAGTCTGG--CTGTGCCCAAGGCTGGAGTGACAGCGGCGGTGATTCACAGTTCACTGCAG	1164
Db	33205	ACAGAGTTTCATTCTGTCAACCAGGCTGGAGTGTAGTGTGTGATCTTGGCTCACTGCACA	33264
OY	1165	CCTCAACTTCTTAGGCTCAAGGGATTCTCCCACTCAGCCCCCAAGTAGTTGGAGCAC	1224
Db	33265	CCTGTGCTCCAGGTTGAAGCGATTCTCCAGCCTCAGCCTCCGAGTAGCTGGGATTAG	33324
OY	1225	ACGTATGCGCCACCATGCGCTGGGCTAAATTCTTAATTTTTGTAGATAGATCTCACTA	1284
Db	33325	AGGCATGTGCCACCATGCGCTGGGCTAATTTTGTATTTTGTAGAGACAGGATTTACACA	33384
OY	1285	TATTGTCCAGGCTGTCTTGAATTCCTGGGCTCAGGTGAGCCTCCACTGGGCTTCCA	1344
Db	33385	TGTTGCTCAGGCTGGTCTTGAACTCTCGACCTCAAGTGATCCACTGCGCTCAGCCTCCA	33444
OY	1345	AAGTACTGGGATTCACAGGCATGAGCCAAAGTCCCCTGCC	1383
Db	33445	AAGTCTGGGATTCACAGCATGAGCCATTTGTGCCCAGCC	33483

RESULT 7

US-11-157-389-1/c
; Sequence 1, Application US/11157389
; Publication No. US20050266481A1

; GENERAL INFORMATION:
 ; APPLICANT: Ruddy, David A.
 ; APPLICANT: Wolff, Roger K.
 ; TITLE OF INVENTION: POLYMORPHISMS IN THE REGION OF THE HUMAN
 ; TITLE OF INVENTION: HEMOCHROMATOSIS GENE
 ; NUMBER OF SEQUENCES: 26
 ; CORRESPONDENCE ADDRESS:
 ;

ADDRESSEE: Pennie & Edmonds, LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY

COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE

```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSBQ for Windows Version 2.0b

```

APPLICATION NUMBER: US/11/157,389
FILING DATE: 20-June-2005
CLASSIFICATION:

APPLICATION NUMBER: US/08/852,495
FILING DATE: 07-MAY-1997
CLASSIFICATION:

APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION

REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0057-9999
TELECOMMUNICATION INFORMATION:

TELEFAX: 650-493-5556
TELEX: 66141 PENNIB
INFORMATION FOR SEQ ID NO: 1:

```

;
;
;
LENGTH: 235033 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

```

US-11-157-389-1

Query Match	5.8%;	Score 208.2;	DB 7;	Length 235033;
Best Local Similarity	75.7%;	Pred. No. 1.1e-34;		
Matches 258;	Conservative 0;	Mismatches 83;	Indels 0;	Gaps 0;

Qy	1062	AATTTTAAATTTTAAATTAATTAATTAATTAATTTTGGAGATGAGTCTGGCTGT	1121
Db	200484	AATTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTTTGAGATGAGTCTCACTGT	200425
Qy	1122	CGCCAGGCTGAGTGCAGCGGCTGATCACAGTTCACTGCAGCCTCAACTTCTAGGCT	1181
Db	200424	CGCCAGGCTGAGTGCAGTGGCATGATCTCAGCTCAATGCATCTGCTCTCCAGGTT	200365
Qy	1182	CAAGGATTCCTCCACCTCAGCCCCCAAGTAGTTGGACCAACGATATGGCCACCATG	1241
Db	200364	CAAGTATCCTCCGCTCAGCCTCCTGAGTAGCTGGATTAACAGTGGGCAACACCAAG	200305
Qy	1242	CCTGGCTAATTTCTTATTTTGTAGAGATAGATCTCATATATGTCCAGGCTGTC	1301
Db	200304	CCTGGCTACTTTTGTATTTTGTAGAGATGAGGTTCAACATTTTGGCCAGGCTGTC	200245
Qy	1302	TTGAATTCCTGGGCTCAGGTGAGCCTCCCACTGGGCTCCCAAAGTACTGGGATTACAG	1361
Db	200244	TTGAATTTCTGACCTCATGTGATCTCTGCTCGGCTCCCAAAGTCTGGGATTACGG	200185
Qy	1362	GCATGAGCCAAAGTCCCCCTGCCCATATGAGATTTCTGTCT	1402
Db	200184	GCTTGATCACTGCGCCAGCCAAACATATCTATATTTTTTTT	200144

RESULT 8

```

US-11-112-908-38/c
; Sequence 38, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; APPLICANT: Davis, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112, 908
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564, 758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575, 978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631, 702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633, 826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 38
; LENGTH: 171162
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-38

```

Query Match	5.8%;	Score 206.8;	DB 7;	Length 171162;
Best Local Similarity	75.7%;	Pred. No. 2e-34;		
Matches 256;	Conservative	0;	Mismatches 82;	Indels 0;
				Gaps 0;

OY	1057	TTTTTAATTTTAAATTTTAATTATTATTTAATTTATTTTGAGATGAGCTCG	1116
Db	46965	TATTTATTATTATTATTATTATTATTATTATTATTATTTTTTGGACAGAGTCTC	46906
OY	1117	GCTGTGCCCAAGCTGAGTCAGCGCGCTGAATCACAGTTCACTGCAGCCCTCAACTTCT	1176
Db	46905	ACTGTTGGCCAAGCTGAGTAGACAGTGCATGATCTCGGCTCATCTGCACACTTTGCCCTCCC	46846
OY	1177	AGGCTCAAGGATTTCTCCACCCTCAGCCCCCAAAGTAGTTGGGACACACGTATGCGCCA	1236
Db	46845	GCGCTCAAGCAATTCTCTCGCCTCAGCCCTCCTGAGTAGCTGAGATTACGGGTGTGTGCCA	46786
OY	1237	CCATG CCTG GCTAATTTCTTAATTTTGTGAGATAAGATCTCACTAATTTGTCCAGGC	1296
Db	46785	CCATGCC CAGCTAATTTTGTATTTTGTAGTAGACAGGGTTTCCATGTTGGCCAGGC	46726

[illegible]

RESULT 9

```

US-10-995-561-13312
; Sequence 13312, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS
; TITLE OF INVENTION: CARDIOVASCULAR DISOR
; TITLE OF INVENTION: DETECTION AND USES T
; FILE REFERENCE: CLO01559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13312
; LENGTH: 130472
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-13312

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Query Match 5.8%; Score 206.4; DB 6; Length 130472;

Best Local Similarity	76.8%;	Pred. No. 2.2e-34;
Matches 252;	Conservative 0;	Mismatches 76;
		Indels 0;
		Gaps 0;

QY	1059	TTTAATTTTTAAATTTTTTAAATTATTATTATTTAATTTATTTTGTGAGATGGAGCTGGC	1118
Dp	8086	TTAATTATTGTTAATTATAATTATTATTATTACTAATTTATTTTGAACAGACCAGAAC	8145
QY	1119	TGTGCCCCAGCGCTGAGTGACAGCGCGGTGATCAAGTTCACTGCAGCCTCAACTTCTAG	1178
Dp	8146	TGTCCTCCAGGCTGAGTGACAGTGTGCGATCTTGCGCTCACTGCAGCCTCACCTCCAG	8205
QY	1179	GCTCAAGGATTTCTCCACCTCAGCCCCCAAAGTAGTTGGACCACACGTATGCCAAC	1238
Dp	8206	GCTGAAGTATATCAATGCTCAGCCTCCCGAGTAGCTGGGATTACTGCGTGCAACAC	8265
QY	1239	ATGCTGCGCTAATTTCTAATTTTTTTGTAGAGATAGATCTCACTATATTGTCCAAGCTG	1298
Dp	8266	ACGCCCGGCTAATTTTGTATTTTGTAGAGACAAGGTTTCAACCATGTTGGCCAGGCTG	8325
QY	1299	GTTCTGAATTCCTGGGCTCAGGTGAGCCTCCCACTGGGCTCCCAAGTACTGGGATTA	1358
Dp	8326	GTCTAGAATCTCTGGGCTCATGTGATCCACCCTGGGCTCCCAAGTCTGAGATTA	8385
QY	1359	CAGGCATGAGCCAAAGTCCCCTGCCCAT	1386
Dp	8386	CAGGCATGAGCCAGTGTGCCCAACTGAT	8413

RESULT 10

```

US-11-121-086-8
; Sequence 8, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3

```

; SEQ ID NO 8
; LENGTH: 246960
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-8

Query Match 5.7%; Score 204.4; DB 7; Length 246960;
Best Local Similarity 70.1%; Pred. No. 7.6e-34;
Matches 289; Conservative 0; Mismatches 121; Indels 2; Gaps 1;

QY 994 CTATTTGTATCTAAGTATCACTTGATGTAGACTGGGTAGACAGGTGAACAATATC 1053
Db 174347 CCATGTGGGAAGCTGGCAGCCACAATACCTCAGACTTATCAGATCCACAAGTGAATT 174406
QY 1054 AGTTTTTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTT 1113
Db 174407 TTTTCTTTCTTTCTTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 174466
QY 1114 CTGGCTG--TCGCCAGGCTGAGTGCAGCGCGGTGATCAGTTCAGTGCAGCTCAAC 1171
Db 174467 CTCGCTTCTTTGCCAGGCTGAGTGCAGTGGCGCGATCTCTGCTCACTGCACACTCCGC 174526
QY 1172 CTTCTAGGCTCAAGGATCTCCCACTCAGCCCCCAGTAGTGGGACACACGTATG 1231
Db 174527 CTCCAGGTTCAAGCAATCTCTGCTCAGCTCAGAGTACGTTGAGTACAGGACG 174586
QY 1232 CGCCACCATGCTGCTGCTAATTTCTAATTTTGTAGAGTAGATCTCACTATATCTC 1291
Db 174587 TGCCAGCATGCTGCTGCTAATTTTGTATTTTGTAGAGTAGAGTTCACCATCTTGGT 174646
QY 1292 CAGGCTGCTTGAATTCCTGCGCTCAGGTAGCCTCCCACTGGGCTCCCAAGTACT 1351
Db 174647 CAGGCTGCTTGAATTCCTGCGCTCAGGTAGCCTCCCACTGGGCTCCCAAGTACT 174706
QY 1352 GGGATTACAGGATGAGCCAGGTCCTGCCCCATATGAGATTTCTGCTC 1403
Db 174707 GGGATTACAGGATGAGCCAGGTCCTGCCCCATATGAGATTTCTGCTC 174758

RESULT 11
US-10-928-446A-1
; Sequence 1, Application US/10928446A
; Publication No. US20050277123A1
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF UTAH RESEARCH FOUNDATION
; TITLE OF INVENTION: VARIANTS OF NEDD4L ASSOCIATED WITH HYPERTENSION AND
; TITLE OF INVENTION: VIRAL BUDDING
; FILE REFERENCE: 0274-5785.1US
; CURRENT APPLICATION NUMBER: US/10/928,446A
; PRIOR FILING DATE: 2004-08-26
; PRIOR APPLICATION NUMBER: 60/359,741
; NUMBER OF SEQ ID NOS: 202
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1080000
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: (825234)
; OTHER INFORMATION: the 'n' at position 825234 may be 'c' or 't'
; FEATURE:
; NAME/KEY: allele
; LOCATION: (825270)
; OTHER INFORMATION: the 'n' at position 825270 may be 'c' or 'g'
; FEATURE:
; NAME/KEY: allele
; LOCATION: (825401)
; OTHER INFORMATION: the 'n' at position 825401 may be 'c' or 'a'
; FEATURE:
; NAME/KEY: allele
; LOCATION: (825428)

; OTHER INFORMATION: the 'n' at position 825428 may be 'g' or 'a'
; FEATURE:
; NAME/KEY: allele
; LOCATION: (825473)
; OTHER INFORMATION: the 'n' at position 825473 may be 'g' or 'a'
; FEATURE:
; NAME/KEY: allele
; LOCATION: (825765)
; OTHER INFORMATION: a "c" may be deleted at this position
; FEATURE:
; NAME/KEY: allele
; LOCATION: (825828)
; OTHER INFORMATION: the 'n' at position 825828 may be 'c' or 't'
; FEATURE:
; NAME/KEY: allele
; LOCATION: (826041)
; OTHER INFORMATION: the 'n' at position 826041 may be 'a' or 'g'
; FEATURE:
; NAME/KEY: allele
; LOCATION: (826546)
; OTHER INFORMATION: the 'n' at position 826546 may be 'a' or 'g'
; FEATURE:
; NAME/KEY: allele
; LOCATION: (826654)
; OTHER INFORMATION: the 'n' at position 826654 may be 'a' or 'g'
; FEATURE:
; NAME/KEY: allele
; LOCATION: (826826)
; OTHER INFORMATION: the 'n' at position 826826 may be 'a' or 'g'
; FEATURE:
; NAME/KEY: allele
; LOCATION: (826863)
; OTHER INFORMATION: the 'n' at position 826863 may be 'a' or 'g'
; FEATURE:
; NAME/KEY: allele
; LOCATION: (827008)
; OTHER INFORMATION: the 'n' at position 827008 may be 'a' or 'g'
; FEATURE:
; NAME/KEY: allele
; LOCATION: (843055)
; OTHER INFORMATION: the 'n' at position 843055 may be 'g' or 'a'
; FEATURE:
; NAME/KEY: allele
; LOCATION: (843118)
; OTHER INFORMATION: the 'n' at position 843118 may be 'c' or 'c'
; FEATURE:
; NAME/KEY: allele
; LOCATION: (871027)
; OTHER INFORMATION: the 'n' at position 871027 may be 'a' or 'g'
; FEATURE:
; NAME/KEY: allele
; LOCATION: (871140)
; OTHER INFORMATION: the 'n' at position 871140 may be 'c' or 't'
; FEATURE:
; NAME/KEY: allele
; LOCATION: (871168)
; OTHER INFORMATION: the 'n' at position 871168 may be 'c' or 'a'
; FEATURE:
; NAME/KEY: allele
; LOCATION: (872678)
; OTHER INFORMATION: the 'n' at position 872678 may be 'c' or 't'
; FEATURE:
; NAME/KEY: allele
; LOCATION: (872742)
; OTHER INFORMATION: the 'n' at position 872742 may be 'a' or 'g'
; FEATURE:
; NAME/KEY: allele
; LOCATION: (925859)
; OTHER INFORMATION: the 'n' at position 925859 may be 'c' or 'g'
; FEATURE:
; NAME/KEY: allele
; LOCATION: (993220)
; OTHER INFORMATION: the 'n' at position 993220 may be 'c' or 't'

```

FEATURE:
NAME/KEY: allele
LOCATION: (993254)
OTHER INFORMATION: the 'n' at position 993254 may be 'g' or 'a'
FEATURE:
NAME/KEY: allele
LOCATION: (1006462)
OTHER INFORMATION: the 'n' at position 1006462 may be 'c' or 't'
FEATURE:
NAME/KEY: allele
LOCATION: (1007820) ..(1007823)
OTHER INFORMATION: "ttct" may be deleted at this position
FEATURE:
NAME/KEY: allele
LOCATION: (1018038)
OTHER INFORMATION: the 'n' at position 1018038 may be 'a' or 'g'
FEATURE:
NAME/KEY: allele
LOCATION: (1018704)
OTHER INFORMATION: the 'n' at position 1018704 may be 'c' or 't'
FEATURE:
NAME/KEY: allele
LOCATION: (1018718) ..(1018720)
OTHER INFORMATION: "gtc" may be deleted at this position
FEATURE:
NAME/KEY: allele
LOCATION: (1026786)
OTHER INFORMATION: the 'n' at position 1026786 may be 'c' or 'a'
FEATURE:
NAME/KEY: allele
LOCATION: (1047134)
OTHER INFORMATION: the 'n' at position 1047134 may be 'a' or 'g'
FEATURE:
NAME/KEY: allele
LOCATION: (1047159)
OTHER INFORMATION: the 'n' at position 1047159 may be 'a' or 'g'
FEATURE:
NAME/KEY: allele
LOCATION: (1047378)
OTHER INFORMATION: the 'n' at position 1047378 may be 'c' or 't'
FEATURE:
NAME/KEY: allele
LOCATION: (1047739)
OTHER INFORMATION: the 'n' at position 1047739 may be 'a' or 'g'
FEATURE:
NAME/KEY: allele
LOCATION: (1050133) ..(1050137)
OTHER INFORMATION: "ttaaa" may be deleted at this position
FEATURE:
NAME/KEY: allele
LOCATION: (1050539)
OTHER INFORMATION: the 'n' at position 1050539 may be 'c' or 't'
FEATURE:
NAME/KEY: allele
LOCATION: (1062808)
OTHER INFORMATION: the 'n' at position 1062808 may be 'c' or 'g'
FEATURE:
NAME/KEY: allele
LOCATION: (1066392)
OTHER INFORMATION: the 'n' at position 1066392 may be 'a' or 'g'
FEATURE:
NAME/KEY: allele
LOCATION: (1073711)
OTHER INFORMATION: the 'n' at position 1073711 may be 'c' or 't'
US-10-928-446A-1

```

Query Match	5.7%;	Score 204.2;	DB 6;	Length 1080000;
Best Local Similarity	76.3%;	Pred. No. 1.6e-33;		
Matches 251; Conservative	0;	Mismatches 78;	Indels 0;	Gaps 0;

QY 1059 TTTAATTTTTTAATTTTTTAAATTATTTATTTATTTTGAGATGAGTCGTGC 1118
|| ||| | ||| ||||||||| ||| |||
Db 960173 TTATTTATTTATTTATTTATTTATTTATTTATTTAGACTGTCTCGCTC 960232

QY	1119	TGTGCCCCAGGCTGAGTGCAGCGGGCGTGATCACAAGTTCACTGCAGCCTTCAACTTCTAG	1178
Db	960233	TGTGCCCCAGGCTGAGCGCAGATGGTGCATCTCAGCTCACTGCACACTTCCACTTCCCGG	9602922
QY	1179	GCTCAAGGGAATCTCCCACTCAGCCCCCAAGTAGTTGGGACCACACGTATGCCCAACC	1238
Db	960293	GTTCAAGCGAATCTCCTGCCTTAGCCTCCCTGAGTAGCTGGGATTACAGGTGCACGCCACC	9603522
QY	1239	ATGCTGGCTAATTTCTAATTTTTTGTAGAGATGAGATCTCACTAATATGTCCAGGCTG	1298
Db	960353	ACACCTGGCTAATTTCTGTATTTTAGTAGAGACGGGGTTTCAACCATGTGGTCAGGCTG	9604122
QY	1299	GTTCTGAATTCCTGGGCTCAGGTGAGCCTCCCACTGGGGCTCCCAAGTACTGGGATTA	1358
Db	960413	GTCTCAAACTCTCTGACCTCAGGTGATCCACCCGGCTCTGGGCTCCCAAGTCTGGGATTA	9604722
QY	1359	CAGGCATGAGCCCAAGGTCCCTGCCCATTA	1387
Db	960473	CAGGCGTGAGCCCAACCATGCCCCAGCCCATTA	960501

RESULT 12
US-10-928-446A-181
; Sequence 181, Application US/10928446A
; Publication No. US20050277123A1

```

: APPLICANT: UNIVERSITY OF UTAH RESEARCH FOUNDATION
: TITLE OF INVENTION: VARIANTS OF NEDD4L ASSOCIATED WITH HYPERTENSION AND
: TITLE OF INVENTION: VIRAL BUDDING
: FILE REFERENCE: 0274-5785.1US
: CURRENT APPLICATION NUMBER: US/10/928,446A
: CURRENT FILING DATE: 2004-08-26
: PRIOR APPLICATION NUMBER: 60/359,741
: PRIOR FILING DATE: 2002-02-26
: NUMBER OF SEQ ID NOS: 202
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 181
: LENGTH: 1080000
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (826985)..(827008)
: FEATURE:
: OTHER INFORMATION: full exon 1 range is 826667-827008
: FEATURE:
: NAME/KEY: allele
: LOCATION: (827008)..(827008)
: OTHER INFORMATION: the 'n' at position 827008 may be 'a' or 'g'
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (843242)..(843315)
: OTHER INFORMATION: exon
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (922549)..(922630)
: OTHER INFORMATION: exon
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (926021)..(926059)
: OTHER INFORMATION: exon
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (929123)..(929176)
: OTHER INFORMATION: exon
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (993104)..(993154)
: OTHER INFORMATION: exon
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (999547)..(999608)

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1 OTHER INFORMATION: exon
2 FEATURE:
3 NAME/KEY: CDS
4 LOCATION: (1000354) .. (1000456)
5 OTHER INFORMATION: exon
6 FEATURE:
7 NAME/KEY: CDS
8 LOCATION: (1002118) .. (1002284)
9 OTHER INFORMATION: exon
10 FEATURE:
11 NAME/KEY: CDS
12 LOCATION: (1006117) .. (1006249)
13 OTHER INFORMATION: exon
14 FEATURE:
15 NAME/KEY: CDS
16 LOCATION: (1007860) .. (1008036)
17 OTHER INFORMATION: exon
18 FEATURE:
19 NAME/KEY: CDS
20 LOCATION: (1010940) .. (1011014)
21 OTHER INFORMATION: exon
22 FEATURE:
23 NAME/KEY: CDS
24 LOCATION: (1018160) .. (1018291)
25 OTHER INFORMATION: exon
26 FEATURE:
27 NAME/KEY: CDS
28 LOCATION: (1018800) .. (1018919)
29 OTHER INFORMATION: exon
30 FEATURE:
31 NAME/KEY: CDS
32 LOCATION: (1020028) .. (1020225)
33 OTHER INFORMATION: exon
34 FEATURE:
35 NAME/KEY: CDS
36 LOCATION: (1026659) .. (1026736)
37 OTHER INFORMATION: exon
38 FEATURE:
39 NAME/KEY: CDS
40 LOCATION: (1028113) .. (1028167)
41 OTHER INFORMATION: exon
42 FEATURE:
43 NAME/KEY: CDS
44 LOCATION: (1034316) .. (1034374)
45 OTHER INFORMATION: exon
46 FEATURE:
47 NAME/KEY: CDS
48 LOCATION: (1041390) .. (1041455)
49 OTHER INFORMATION: exon
50 FEATURE:
51 NAME/KEY: CDS
52 LOCATION: (1043121) .. (1043350)
53 OTHER INFORMATION: exon
54 FEATURE:
55 NAME/KEY: CDS
56 LOCATION: (1044868) .. (1044989)
57 OTHER INFORMATION: exon
58 FEATURE:
59 NAME/KEY: CDS
60 LOCATION: (1047519) .. (1047589)
61 OTHER INFORMATION: exon
62 FEATURE:
63 NAME/KEY: CDS
64 LOCATION: (1050296) .. (1050391)
65 OTHER INFORMATION: exon
66 FEATURE:
67 NAME/KEY: CDS
68 LOCATION: (1060368) .. (1060441)
69 OTHER INFORMATION: exon
70 FEATURE:
71 NAME/KEY: CDS
72 LOCATION: (1062648) .. (1062708)
73 OTHER INFORMATION: exon

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? FEATURE:
? NAME/KEY: CDS
? LOCATION: (1064561)..(1064620)
? OTHER INFORMATION: exon
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (1066207)..(1066314)
? OTHER INFORMATION: exon
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (1067768)..(1067864)
? OTHER INFORMATION: exon
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (1068609)..(1068681)
? OTHER INFORMATION: exon
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (1073289)..(1073388)
? FEATURE:
? OTHER INFORMATION: full exon 30 range is 1073289-1075279
US-10-928-446A-181

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Query Match	5.7%	Score 204.2;	DB 6;	Length 1080000;
Best Local Similarity	76.3%	Pred. No. 1.6e-33;		
Matches 251; Conservative	0;	Mismatches 78;	Indels 0;	Gaps 0;

QY	1059	TTTAATTTTTAATTTTTTAAATTATTATTATTATTATTATTATTATTATTGAGATGAGCTGGC	1118
Dp	960173	TTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTAGACTGTCTCGCTC	960232
QY	1119	TGTGCCCCAGGCTGAGGTGCAGCGGCGGTGATCACAGTTCACTGCAGCCTCAACCTTCTAG	1178
Dp	960233	TGTGCCCCAGGCTGAGGCGCAGTGGTGCGMTCTCAGCTCACTGCAACCTTCACCTTCCGG	960292
QY	1179	GCTCAAGGGAATTCGCCAACCTCAGCCCCCAAAGTAGTTGGACCACACGTAATGCCACC	1238
Dp	960293	GTTCAAGCAATCTCTGCTTAGCCTCCTGAGTAGCTGGGATTACAGGTGACGCCACC	960352
QY	1239	ATGCGTGGCTAATTTCTAATTTTTTTGTADAGATAGATCTCACTATATTGTCCAGCTG	1298
Dp	960353	ACACCTGGCTAATTTCTGTATTTTGTAGTAGAGCGGGTTTCACCATGTTGTGAGGCTG	960412
QY	1299	GTCTTGAATTCCTGGGCTCAGGTGAGCCTCCCACTGGGCTCCCAAAGTACTGGGATTA	1358
Dp	960413	GTCTCAAACTCCTGAACCTCAGGTGATCCACCCGCGCTCGGCTCCCAAAGTGTGGATTA	960472
QY	1359	CAGGCATGAGCCAGAAGTCCCCTGCCCATTA	1387
Dp	960473	CAGGCGTAGCCACCATGCCCCAGCCCATTA	960501

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RESULT 13
US-10-928-446A-183
; Sequence 183, Application US/10928446A
; Publication No. US20050277123A1
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF UTAH RESEARCH FOUNDATION
; TITLE OF INVENTION: VARIANTS OF NEDD4L ASSOCIATED WITH HYPERTENSION AND
; TITLE OF INVENTION: VIRAL BUDDING
; FILE REFERENCE: 0274-5785.1US
; CURRENT APPLICATION NUMBER: US/10/928,446A
; CURRENT FILING DATE: 2004-08-26
; PRIOR APPLICATION NUMBER: 60/359,741
; PRIOR FILING DATE: 2002-02-26
; NUMBER OF SEQ ID NOS: 202
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 183
; LENGTH: 1080000
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS

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/ LOCATION: (826985)..(827017)
/ FEATURE:
/ OTHER INFORMATION: full exon 1 range is 826667-827008
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (843242)..(843315)
/ OTHER INFORMATION: exon
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (922549)..(922630)
/ OTHER INFORMATION: exon
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (926021)..(926059)
/ OTHER INFORMATION: exon
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (929123)..(929176)
/ OTHER INFORMATION: exon
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (993104)..(993154)
/ OTHER INFORMATION: exon
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (999547)..(999608)
/ OTHER INFORMATION: exon
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1000354)..(1000456)
/ OTHER INFORMATION: exon
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1002118)..(1002284)
/ OTHER INFORMATION: exon
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1006117)..(1006249)
/ OTHER INFORMATION: exon
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1007860)..(1008036)
/ OTHER INFORMATION: exon
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1010940)..(1011014)
/ OTHER INFORMATION: exon
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1018160)..(1018291)
/ OTHER INFORMATION: exon
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1018800)..(1018919)
/ OTHER INFORMATION: exon
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1020028)..(1020225)
/ OTHER INFORMATION: exon
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1026659)..(1026736)
/ OTHER INFORMATION: exon
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1028113)..(1028167)
/ OTHER INFORMATION: exon
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1034316)..(1034374)
/ OTHER INFORMATION: exon
/ FEATURE:
/ NAME/KEY: CDS

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; LOCATION: (1041390)..(1041455)
; OTHER INFORMATION: exon
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1043121)..(1043350)
; OTHER INFORMATION: exon
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1044868)..(1044989)
; OTHER INFORMATION: exon
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1047519)..(1047589)
; OTHER INFORMATION: exon
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1050296)..(1050391)
; OTHER INFORMATION: exon
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1060368)..(1060441)
; OTHER INFORMATION: exon
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1062648)..(1062708)
; OTHER INFORMATION: exon
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1064561)..(1064620)
; OTHER INFORMATION: exon
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1066207)..(1066314)
; OTHER INFORMATION: exon
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1067768)..(1067864)
; OTHER INFORMATION: exon
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1068609)..(1068681)
; OTHER INFORMATION: exon
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1073289)..(1073388)
; FEATURE:
; OTHER INFORMATION: full exon 30 range is 1073289-1075279
; US-10-928-446A-183

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[illegible]

QY 1359 CAGCATGAGCCAGGTCCCTGCCCATTA 1387
Db 960473 CAGCGGTGAGCCACCATGCCCGCCCATTA 960501

RESULT 14

US-10-928-446A-185
; Sequence 185, Application US/10928446A
; Publication No. US20050277123A1
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF UTAH RESEARCH FOUNDATION
; TITLE OF INVENTION: VARIANTS OF NEDD4L ASSOCIATED WITH HYPERTENSION AND
; TITLE OF INVENTION: VIRAL BUDDING
; FILE REFERENCE: 0274-5785.1US
; CURRENT APPLICATION NUMBER: US/10/928,446A
; PRIOR FILING DATE: 2004-08-26
; PRIOR FILING DATE: 2002-02-26
; NUMBER OF SEQ ID NOS: 202
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 185
; LENGTH: 1080000
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (722487)..(722534)
; FEATURE:
; OTHER INFORMATION: full length exon 1 range is 722213-722534
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (843242)..(843315)
; OTHER INFORMATION: exon
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (922549)..(922630)
; OTHER INFORMATION: exon
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (926021)..(926059)
; OTHER INFORMATION: exon
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (929123)..(929176)
; OTHER INFORMATION: exon
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (993104)..(993154)
; OTHER INFORMATION: exon
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (999547)..(999608)
; OTHER INFORMATION: exon
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1000354)..(1000456)
; OTHER INFORMATION: exon
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1002118)..(1002284)
; OTHER INFORMATION: exon
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1006117)..(1006249)
; OTHER INFORMATION: exon
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1007860)..(1008036)
; OTHER INFORMATION: exon
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1010940)..(1011014)
; OTHER INFORMATION: exon
;

;; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1018160)..(1018291)
; OTHER INFORMATION: exon
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1018800)..(1018919)
; OTHER INFORMATION: exon
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1020028)..(1020225)
; OTHER INFORMATION: exon
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1026659)..(1026736)
; OTHER INFORMATION: exon
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1028113)..(1028167)
; OTHER INFORMATION: exon
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1034316)..(1034374)
; OTHER INFORMATION: exon
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1041390)..(1041455)
; OTHER INFORMATION: exon
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1043121)..(1043350)
; OTHER INFORMATION: exon
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1044868)..(1044989)
; OTHER INFORMATION: exon
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1047519)..(1047589)
; OTHER INFORMATION: exon
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1050296)..(1050391)
; OTHER INFORMATION: exon
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1060368)..(1060441)
; OTHER INFORMATION: exon
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1062648)..(1062708)
; OTHER INFORMATION: exon
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1064561)..(1064620)
; OTHER INFORMATION: exon
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1066207)..(1066314)
; OTHER INFORMATION: exon
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1067768)..(1067864)
; OTHER INFORMATION: exon
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1068609)..(1068681)
; OTHER INFORMATION: exon
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1073289)..(1073388)
; OTHER INFORMATION: full length exon 30 range is 1073289-1075279
;

US-10-928-446A-185

Query Match	5.7%;	Score 204.2;	DB 6;	Length 1080000;
Best Local Similarity	76.3%;	Pred. No. 1.6e-33;		
Matches 251; Conservative	0;	Mismatches 78;	Indels 0;	Gaps 0;

OY	1059	TTTAATTTTTTAAATTTTAAATAATTATTTATTTATTTATTTTGAGATGGAGTCGTGGC	1118
Dd	960173	TTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTGAGACTGTGTCTCGCTC	960232
OY	1119	TGTCGCCAGGCTGGAGTGCAGCGCGCTGATCACAGTTCACTGCAGCCTCAACCTTCTAG	1178
Dd	960233	TGTCGCCAGGCTGGAGCGCAGTGTGCGATCTCAGCTCACTGCMAACCTCCACTTCCCGG	960292
OY	1179	GCTCAAAGGATTTCTCCACCCTCAGCCCCCAAGTAGTTGGGACACACGTATGCGCCACC	1238
Dd	960293	GTTCAAGGATTTCTCCTGCCTTAGCCTCCTGAGTAGTGGGATTACAGGTGCACGCCACC	960352
OY	1239	ATGCTGTGCTAATTTCTTAATTTTTTGTAGAGATAGATCTCACTAATTTGTCCAGGCTG	1298
Dd	960353	ACAACCTGGCTAATTTCTGTATTTTAAAGTAGAGACGGGGTTTCAACCATGTTGGTCAGGCTG	960412
OY	1299	GTC TTGAATTCCTGGGCTCAGGTGAGCCTCCCACTGGGCTCCCAAAGTA CTGGGATTA	1358
Dd	960413	GTCTCAAATCTCTGACCTCAGGTGATCCACCCGCTCGGCTCCCAAAGTGTGGGATTA	960472
OY	1359	CAGGCATGAGCCAAGGTCCCTGCCCATA	1387
Dd	960473	CAGGCGTGAGCCCAACCATGCCCCAGCCATA	960501

RESULT 15
US-10-928-446A-187

Sequence 187, Application US/10928446A

Publication No. US20050277123A1

GENERAL INFORMATION:

APPLICANT: UNIVERSITY OF UTAH RESEARCH FOUNDATION

TITLE OF INVENTION: VARIANTS OF NEDDAL ASSOCIATED WITH HYPERTENSION AND

TITLE OF INVENTION: VIRAL BUDDING

FILE REFERENCE: 0274-5785.1US

CURRENT	APPLICATION	NUMBER:	US/11
ATTORNEY	FITTING	0004	00 00

CURRENT FILING DATE: 2004-08-26

PRIOR APPLICATION NUMBER: 6
 PRIOR FILING DATE: 2003 03

PRIOR FILING DATE: 2002-02-
NUMBER OF SEQ ID NOS: 203

NUMBER OF SE
COUNTABLE. D

SOFTWARE: Patent
SEQ ID NO 187

SEQ ID NO 1
LENGTH: 7

LENGTH: 1080000
TYPE: DNA

**LIFE: DI
ORGANISM**

FEATURE:

NAME/KEY: CDS

LOCATION

FEATURE: ()

OTHER IN

FEATURE:

NAME/KEY: CDS

LOCATION: (1000354) .. (1

OTHER IN

FEATURE:

NAME/KEY: CDS

LOCATION: (1002118) ..(1

OTHER IN

FEATURE:

NAME/KEY: CDS
LOCATION: (1006117) (1006348)

LOCATION: (1006117) ..(1

OTHER IN
FEATURE

NAME/KEY: CDS

NAME/KEY: CDS
LOCATION: (1007860) - (1008036)

LOCATION: (100/880) .. (1
OTHER INFORMATION: exon

OTHER FEATURES:

NAME/KEY: CDS

08/06/2017

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1 LOCATION: (1010940)..(1011014)
2 OTHER INFORMATION: exon
3 FEATURE:
4 NAME/KEY: CDS
5 LOCATION: (1018160)..(1018291)
6 OTHER INFORMATION: exon
7 FEATURE:
8 NAME/KEY: CDS
9 LOCATION: (1018800)..(1018919)
10 OTHER INFORMATION: exon
11 FEATURE:
12 NAME/KEY: CDS
13 LOCATION: (1020028)..(1020225)
14 OTHER INFORMATION: exon
15 FEATURE:
16 NAME/KEY: CDS
17 LOCATION: (1026659)..(1026736)
18 OTHER INFORMATION: exon
19 FEATURE:
20 NAME/KEY: CDS
21 LOCATION: (1028113)..(1028167)
22 OTHER INFORMATION: exon
23 FEATURE:
24 NAME/KEY: CDS
25 LOCATION: (1034316)..(1034374)
26 OTHER INFORMATION: exon
27 FEATURE:
28 NAME/KEY: CDS
29 LOCATION: (1041390)..(1041455)
30 OTHER INFORMATION: exon
31 FEATURE:
32 NAME/KEY: CDS
33 LOCATION: (1043121)..(1043350)
34 OTHER INFORMATION: exon
35 FEATURE:
36 NAME/KEY: CDS
37 LOCATION: (1044868)..(1044989)
38 OTHER INFORMATION: exon
39 FEATURE:
40 NAME/KEY: CDS
41 LOCATION: (1050296)..(1050391)
42 OTHER INFORMATION: exon
43 FEATURE:
44 NAME/KEY: CDS
45 LOCATION: (1060368)..(1060411)
46 OTHER INFORMATION: exon
47 FEATURE:
48 NAME/KEY: CDS
49 LOCATION: (1062648)..(1062708)
50 OTHER INFORMATION: exon
51 FEATURE:
52 NAME/KEY: CDS
53 LOCATION: (1064561)..(1064620)
54 OTHER INFORMATION: exon
55 FEATURE:
56 NAME/KEY: CDS
57 LOCATION: (1066207)..(1066314)
58 OTHER INFORMATION: exon
59 FEATURE:
60 NAME/KEY: CDS
61 LOCATION: (1067768)..(1067864)
62 OTHER INFORMATION: exon
63 FEATURE:
64 NAME/KEY: CDS
65 LOCATION: (1068609)..(1068681)
66 OTHER INFORMATION: exon
67 FEATURE:
68 NAME/KEY: CDS
69 LOCATION: (1073289)..(1073388)

```

FEATURE:
; OTHER INFORMATION: full length exon 30 range is 1073289-1075279
US-10-928-446A-187

Query Match 5.7%; Score 204.2; DB 6; Length 1080000;
Best Local Similarity 76.3%; Pred. No. 1.6e-33;
Matches 251; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

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QY 1059 TTTAATTTTAAATTTTAAATTTAATTTAATTTAATTTAATTTTGAAGATGAGCTGGC 1118
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 960173 TTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAAGACTGTGTCTGCTC 960232

QY 1119 TGTGCCCCAGGCTGAGTGCAGCGCGGTGATCAAGTTCACTGCAGCCTCAACCTTCTAG 1178
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 960233 TGTGCCCCAGGCTGAGCGCAGTGTGCGATCTCAGCTCACTGCACCTCCACTTCCCGG 960292

QY 1179 GTCAGAGGATTTCTCCCACTCAGCCCCCAAGTAGTTGGGACCAACGTATGCGCACCC 1238
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 960293 GTTCAAGCGATTCTCCGTGCTTAGCCTCTGAGTAGCTGGGATTACAGGTGCACGCGCACCC 960352

QY 1239 ATGCTGGCTAATTTCTTATTTTGTAGAGATGATCTCACTATATTGTCCAGGCTG 1298
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 960353 ACACCTGGCTAATTTCTGTATTTTAGTAGAGACGGGATTTCACCATGTTGTCAGGCTG 960412

QY 1299 GTCTGAATTCCTGGGCTCAGGTGAGCCTCCCACTGGGCTCCCAAGTACTGGGATTA 1358
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 960413 GTCTCAACTCCTGACCTCAGGTGATCCACCGGCTCGGCTCCCAAGTGTGGGATTA 960472

QY 1359 CAGGCATGAGCCCAAGGTCCCTGCCATA 1387
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 960473 CAGGCGTAGGCCCAACCATGCCCAGCCATA 960501
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Search completed: January 7, 2006, 20:47:43
Job time : 687.111 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 7, 2006, 06:18:20 ; Search time 2602.82 Seconds
(without alignments)
11393.018 Million cell updates/sec

Title: US-10-767-521-3

Perfect score: 3586
Sequence: 1 ggatccctaccttccccatc.....ctatcacaggagaagtga 3586

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA Main:*

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2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
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7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3586	100.0	3586	US-09-922-895-3	Sequence 3, Appli
2	3586	100.0	3586	US-10-767-521-3	Sequence 3, Appli
3	3494.4	97.4	5791	US-10-929-182-21	Sequence 21, Appl
4	3494.4	97.4	5791	US-10-486-471-5	Sequence 5, Appli
5	2406	67.1	7201	US-10-311-455-310	Sequence 310, App
6	2271.8	63.4	7201	US-10-311-455-309	Sequence 309, App
7	344.2	9.6	1915	US-10-106-623-3	Sequence 3, Appli
8	344.2	9.6	1915	US-10-772-037-3	Sequence 727856,
9	215.2	6.0	3771	US-09-925-065A-727856	Sequence 804603,
10	212.4	5.9	606	US-09-925-065A-804603	Sequence 248133,
11	212.2	5.9	582	US-09-925-065A-248133	Sequence 923960,
12	212.2	5.9	726	US-09-925-065A-923960	Sequence 6920, Ap
13	211.8	5.9	13000	US-10-719-993-6920	Sequence 946, App
14	211.8	5.9	54701	US-10-087-192-946	Sequence 6833, Ap
15	211.8	5.9	60316	US-10-719-993-6833	Sequence 53249, A
16	211.4	5.9	1418	US-09-925-065A-53249	Sequence 53250, A
17	211.4	5.9	1418	US-09-925-065A-53250	Sequence 53251, A
18	211.4	5.9	1418	US-09-925-065A-53251	Sequence 53252, A
19	211.4	5.9	1418	US-09-925-065A-53252	Sequence 857329,
20	211.2	5.9	606	US-09-925-065A-857329	Sequence 857330,
21	211.2	5.9	606	US-09-925-065A-857330	Sequence 248131,
22	211	5.9	582	US-09-925-065A-248131	Sequence 248134,
23	211	5.9	582	US-09-925-065A-248134	

24	210.8	5.9	1234	4	US-09-925-065A-696705	Sequence 696705,
25	210.6	5.9	582	4	US-09-925-065A-248132	Sequence 248132,
26	210.6	5.9	102790	7	US-10-367-094-163	Sequence 163, App
27	210.6	5.9	160361	7	US-10-235-192A-35	Sequence 35, Appl
28	210.4	5.9	787	4	US-09-925-065A-936523	Sequence 936523,
29	210.2	5.9	631	4	US-09-925-065A-169305	Sequence 169305,
30	210.2	5.9	168821	5	US-10-087-192-622	Sequence 622, App
31	209.8	5.9	631	4	US-09-925-065A-169304	Sequence 169304,
32	209.8	5.9	657	4	US-09-925-065A-295251	Sequence 295251,
33	209.6	5.8	210	4	US-09-925-065A-349513	Sequence 349513,
34	209.6	5.8	155572	9	US-10-981-277-30	Sequence 30, Appl
35	209.2	5.8	787	4	US-09-925-065A-936524	Sequence 936524,
36	209	5.8	59215	9	US-10-472-929-3	Sequence 3, Appli
37	208.8	5.8	746	4	US-09-925-065A-936526	Sequence 936526,
38	208.8	5.8	746	4	US-09-925-065A-953476	Sequence 953476,
39	208.8	5.8	787	4	US-09-925-065A-936525	Sequence 936525,
40	208.2	5.8	235033	5	US-10-301-844-1	Sequence 1, Appli
41	208	5.8	612	4	US-09-925-065A-940151	Sequence 940151,
42	208	5.8	620	4	US-09-925-065A-926832	Sequence 926832,
43	207.4	5.8	652	5	US-10-027-632-14511	Sequence 14511, A
44	207.4	5.8	652	6	US-10-027-632-14511	Sequence 14511, A
45	206.4	5.8	119501	6	US-10-174-319-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1
US-09-922-895-3

Sequence 3, Application US/09922895
Publication No. US20020192214A1

GENERAL INFORMATION:

APPLICANT: DAUGHERTY, BRUCE L.
DEMARTINO, JULIE A.
SICILIANO, SALVATORE J.
SPRINGER, MARTIN J.

TITLE OF INVENTION: EOSINOPHIL EOTAXIN RECEPTOR
NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000, 126 E. Lincoln Ave.

CITY: Rahway
STATE: NJ

COUNTRY: USA
ZIP: 07065-0900

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/922,895

FILING DATE: 06-Aug-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/847,296

FILING DATE: <Unknown>
APPLICATION NUMBER: 60/017,113

FILING DATE: 26-APR-1996
ATTORNEY/AGENT INFORMATION:

NAME: Thies, J. Eric
REGISTRATION NUMBER: 35,382

REFERENCE/DOCKET NUMBER: 19634Y
TELECOMMUNICATION INFORMATION:

TELEPHONE: 908-594-3904
TELEFAX: 908-594-4720

TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
LENGTH: 3586 base pairs

TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-922-895-3

Query Match 100.0%; Score 3586; DB 3; Length 3586;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3586; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATCCCTACCTTCCCCTCAGAGCTAGGGGGCATGAGCGCTCTGCTAAGATGGGA 60
DB 1 GGATCCCTACCTTCCCCTCAGAGCTAGGGGGCATGAGCGCTCTGCTAAGATGGGA 60
QY 61 CCCCAGGAATGTCTCCCTGTGGGCACTTCCCTACAGATGGATGGCCAGTGCCTT 120
DB 61 CCCCAGGAATGTCTCCCTGTGGGCACTTCCCTACAGATGGATGGCCAGTGCCTT 120
QY 121 AAGTTGTGTGTCAGGCAGAAAAAAGATCTAGTTTGTACTCTTGAGATTCTCGGTTT 180
DB 121 AAGTTGTGTGTCAGGCAGAAAAAAGATCTAGTTTGTACTCTTGAGATTCTCGGTTT 180
QY 181 GTTCATGCGATGGGCAAGGAGTCAAGAGCAGACCCCTTGCTCACTGCTTACCACTGCA 240
DB 181 GTTCATGCGATGGGCAAGGAGTCAAGAGCAGACCCCTTGCTCACTGCTTACCACTGCA 240
QY 241 GGAAGAGTGATAGCCTGTGGCCAGGGCCAGGGCCCTGTGTGAGGGGTAGTGTAAACAGA 300
DB 241 GGAAGAGTGATAGCCTGTGGCCAGGGCCAGGGCCCTGTGTGAGGGGTAGTGTAAACAGA 300
QY 301 GAGGGCTTCCATTCAGCCCAAGGAAGCTAAGAATGAATACCTCATGATATATTAGC 360
DB 301 GAGGGCTTCCATTCAGCCCAAGGAAGCTAAGAATGAATACCTCATGATATATTAGC 360
QY 361 TACAACCAACAAGAGGCTCAGAAAAAGGCTCAGCGTTGGAACAGGTCACCCCCAC 420
DB 361 TACAACCAACAAGAGGCTCAGAAAAAGGCTCAGCGTTGGAACAGGTCACCCCCAC 420
QY 421 TCAGCAGACCAAGTCATATAATCAAGACCAACAGAGACAGAACACCCCTTCCCA 480
DB 421 TCAGCAGACCAAGTCATATAATCAAGACCAACAGAGACAGAACACCCCTTCCCA 480
QY 481 CTCTGCCCCATGTCTCAAGTTGTAGTGGCCCTTCTCCAGATCTCTGCGCAACCATCTTAGA 540
DB 481 CTCTGCCCCATGTCTCAAGTTGTAGTGGCCCTTCTCCAGATCTCTGCGCAACCATCTTAGA 540
QY 541 AAGGAACA CTGAAAAGAACTGAAATTATAAGCTGACAGCATAAAGAGATGATAAA 600
DB 541 AAGGAACA CTGAAAAGAACTGAAATTATAAGCTGACAGCATAAAGAGATGATAAA 600
QY 601 ACCTAAATCATTTGTTCAATGAATGAATCAAGAAATTAAACCACTTTGACTAAAA 660
DB 601 ACCTAAATCATTTGTTCAATGAATGAATCAAGAAATTAAACCACTTTGACTAAAA 660
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DB 661 TGTGTGAATCCTTTTCTCTGCTATCCAGCAGATGAGAAGCTGTAAACAGACCAATA 720
QY 721 GTTTGAGACTTAAAGATCATTTGACATTTCACTGCTGAGTTGTATGTGATTTTA 780
DB 721 GTTTGAGACTTAAAGATCATTTGACATTTCACTGCTGAGTTGTATGTGATTTTA 780
QY 781 GTTGACCTCACTTTGTAAATCTTGACACGCGGCAATCCAATATCTGCACAAGAGATATG 840
DB 781 GTTGACCTCACTTTGTAAATCTTGACACGCGGCAATCCAATATCTGCACAAGAGATATG 840
QY 841 TTAAACAGTGTAAATGCTGCATGAGGAGTTGGGTGATTTTAACTTCTGTTTGTGCT 900
DB 841 TTAAACAGTGTAAATGCTGCATGAGGAGTTGGGTGATTTTAACTTCTGTTTGTGCT 900
QY 901 CTTCTTTCTTATTTCTTACTTATTTACATTAACCTATCGTTTCCCAAAATGTAAAA 960
DB 901 CTTCTTTCTTATTTCTTACTTATTTACATTAACCTATCGTTTCCCAAAATGTAAAA 960
QY 961 GGCCATTTGAAAGCCTAATTCAAACCTTCTTCACTATTTGTATCTAAGTATTCACCTTG 1020

DB 961 GGCCATTTGAAAGCCTAATTCAAACCTTCTTCACTATTTGTATCTAAGTATTCACCTTG 1020
QY 1021 ATTGAGACTGGGTAGACAGGTGAAAAACCATATCAGGTTTAAATTTTAAATTTTAAATT 1080
DB 1021 ATTGAGACTGGGTAGACAGGTGAAAAACCATATCAGGTTTAAATTTTAAATTTTAAATT 1080
QY 1081 ATTATTTAATTTAATTTTATTTTGAATGAGTGTGCTGTGCCCAAGGCTGAGTGACG 1140
DB 1081 ATTATTTAATTTAATTTTATTTTGAATGAGTGTGCTGTGCCCAAGGCTGAGTGACG 1140
QY 1141 CGGCGTATCACAGTTCACTGACGCTCAACCTTCTAGGCTCAAGGATTTCCGACCTC 1200
DB 1141 CGGCGTATCACAGTTCACTGACGCTCAACCTTCTAGGCTCAAGGATTTCCGACCTC 1200
QY 1201 AGCCCCCAAGTAGTTGGACCAACGTAATGCGGCCACCATGCTGCTAATTTCTAATTT 1260
DB 1201 AGCCCCCAAGTAGTTGGACCAACGTAATGCGGCCACCATGCTGCTAATTTCTAATTT 1260
QY 1261 TTTGTAGAGATAGATCTCATATATTGTCCAGGCTGCTTGAATTCCTGGGCTCAGG 1320
DB 1261 TTTGTAGAGATAGATCTCATATATTGTCCAGGCTGCTTGAATTCCTGGGCTCAGG 1320
QY 1321 TGAGCTTCCACCTGGGCTTCCCAAAGTACTGGGATTAAGGATGAGCCAAAGTCCCT 1380
DB 1321 TGAGCTTCCACCTGGGCTTCCCAAAGTACTGGGATTAAGGATGAGCCAAAGTCCCT 1380
QY 1381 GCCCATATGAGATTTTCTGTCTGATCCCATGACGTAGTAATCAAGACTTGGCTGCT 1440
DB 1381 GCCCATATGAGATTTTCTGTCTGATCCCATGACGTAGTAATCAAGACTTGGCTGCT 1440
QY 1441 GACTCTGAGAGACCTGCATGCTTTCTTGAGCTGTGAATTTCAAGTCTAAGTCTATAGG 1500
DB 1441 GACTCTGAGAGACCTGCATGCTTTCTTGAGCTGTGAATTTCAAGTCTAAGTCTATAGG 1500
QY 1501 CAGCCTGAAAACCCAAACCAAAAGGTTCTATGTGTTATCATCTGATCATGTTGATTTA 1560
DB 1501 CAGCCTGAAAACCCAAACCAAAAGGTTCTATGTGTTATCATCTGATCATGTTGATTTA 1560
QY 1561 TAGAATTAACACATGAATTAAGACATACTCCCTCAAACTGAGCAAAACTTAAGTAAATTT 1620
DB 1561 TAGAATTAACACATGAATTAAGACATACTCCCTCAAACTGAGCAAAACTTAAGTAAATTT 1620
QY 1621 TTAAAGTTTGACCTGTTTAAATCACTCTTGAGAAAAAGAAATAAATACAATAA 1680
DB 1621 TTAAAGTTTGACCTGTTTAAATCACTCTTGAGAAAAAGAAATAAATACAATAA 1680
QY 1681 TTAACGTAATTAACAGGCTACTATACCTTTGTTCTCCAGAAATTAAGCACTTCTGTTCTTT 1740
DB 1681 TTAACGTAATTAACAGGCTACTATACCTTTGTTCTCCAGAAATTAAGCACTTCTGTTCTTT 1740
QY 1741 CTTGCTTTAGATGCTGAAGTGAAGAGACACTCTGTGATTTGAAGTGTAACTGACAA 1800
DB 1741 CTTGCTTTAGATGCTGAAGTGAAGAGACACTCTGTGATTTGAAGTGTAACTGACAA 1800
QY 1801 AATGTATATTTTCTCAGCTGCTATGGAATTGATATGCTAATTGAATTAAGATGC 1860
DB 1801 AATGTATATTTTCTCAGCTGCTATGGAATTGATATGCTAATTGAATTAAGATGC 1860
QY 1861 TGATGGAGCACACAAACCAATTTGTTCTCAGTCCATTTCTCCTCAAAAAGCCTGGA 1920
DB 1861 TGATGGAGCACACAAACCAATTTGTTCTCAGTCCATTTCTCCTCAAAAAGCCTGGA 1920
QY 1921 ATGTGCAATTGATCAGTGGAGATGTACCTGACAGACCAATGAAGAGATCAACAAGT 1980
DB 1921 ATGTGCAATTGATCAGTGGAGATGTACCTGACAGACCAATGAAGAGATCAACAAGT 1980
QY 1981 TCACACCAAGGGAACCTATTTTCTTAATTCATTTGAATGGCTTCTAATTTGTTCTT 2040
DB 1981 TCACACCAAGGGAACCTATTTTCTTAATTCATTTGAATGGCTTCTAATTTGTTCTT 2040
QY 2041 TTCAATCTGCTTCTTACAGTTTAAAGCTTTTCTGTTTCAAAATGTGAATCTACATA 2100

Db 2041 TTCAATCTGCTTCCACAGTTTACAGCTTTTCGTGTTCAATGTGAATCACAATA 2100
Qy 2101 CACTCTCATTTTCTCATCAACAACCCCAAGTGACCCCAATGGTCTCACTTTCGATATAA 2160
Db 2101 CACTCTCATTTTCTCATCAACAACCCCAAGTGACCCCAATGGTCTCACTTTCGATATAA 2160
Qy 2161 GTAAAGAGGCTCTGCATTAAGGGCTTGTCCAGAGCAGCAGCTGAGAGGCGCTAGACT 2220
Db 2161 GTAAAGAGGCTCTGCATTAAGGGCTTGTCCAGAGCAGCAGCTGAGAGGCGCTAGACT 2220
Qy 2221 GGCTCCATTTCCATCTCTAATCTCACTGACTTGTGACTACCCAGAACCCCAACATGTGGG 2280
Db 2221 GGCTCCATTTCCATCTCTAATCTCACTGACTTGTGACTACCCAGAACCCCAACATGTGGG 2280
Qy 2281 CCTCAGTATTCGATCAATTAATCTAATTAAGAGCAAAAACAATTTCCCGCATTTGGCCCA 2340
Db 2281 CCTCAGTATTCGATCAATTAATCTAATTAAGAGCAAAAACAATTTCCCGCATTTGGCCCA 2340
Qy 2341 GTTATTAAGCATTCTCAGATTACCTTGAGAAATGCCATGGCCTGTATATTCACATC 2400
Db 2341 GTTATTAAGCATTCTCAGATTACCTTGAGAAATGCCATGGCCTGTATATTCACATC 2400
Qy 2401 TTCAACCTTGTCCCTCCCTAGAAAGAGAAAGTCAAGTGGATGCCCTTGAGGAAT 2460
Db 2401 TTCAACCTTGTCCCTCCCTAGAAAGAGAAAGTCAAGTGGATGCCCTTGAGGAAT 2460
Qy 2461 AGTGCAATGGCTTAATCTGTCTTCCATGACTCCTGCTTATCTGTCTTCTATTTCTCT 2520
Db 2461 AGTGCAATGGCTTAATCTGTCTTCCATGACTCCTGCTTATCTGTCTTCTATTTCTCT 2520
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Db 2521 TTTCACCCGAAAGTCTAATCTCAAGAAAAGCAGGCACTGGCCTTAGGGCTCCTGGCTA 2580
Qy 2581 AGAAATATCAAGTCCAGTGAAGAAATCCCATGACTGACCCCTCTGCTTACCCCTTGTG 2640
Db 2581 AGAAATATCAAGTCCAGTGAAGAAATCCCATGACTGACCCCTCTGCTTACCCCTTGTG 2640
Qy 2641 ATGGAAGAGCTCCAGGGGTTGCTTTTGCATGTACAGGCGCTAATCAGCATCAACA 2700
Db 2641 ATGGAAGAGCTCCAGGGGTTGCTTTTGCATGTGTACAGGCGCTAATCAGCATCAACA 2700
Qy 2701 GGGGCAAGAAAAGAAAGTAACCTAACTAATGCTGTATTAATTTGTAATTTGTAATA 2760
Db 2701 GGGGCAAGAAAAGAAAGTAACCTAACTAATGCTGTATTAATTTGTAATTTGTAATA 2760
Qy 2761 GTTAATTAATGCTGTATTAATTTGTAATTTGTAATTTGTAATTTGTAATTTGTAAT 2820
Db 2761 GTTAATTAATGCTGTATTAATTTGTAATTTGTAATTTGTAATTTGTAATTTGTAAT 2820
Qy 2821 GTGATTTGATTAATGCTGTATTAATTTGTAATTTGTAATTTGTAATTTGTAATTTG 2880
Db 2821 GTGATTTGATTAATGCTGTATTAATTTGTAATTTGTAATTTGTAATTTGTAATTTG 2880
Qy 2881 TCAAGTCCGTAGCAATTTTCAAAAGTTAAATTTAAATTTCACTAATTGAACTAGT 2940
Db 2881 TCAAGTCCGTAGCAATTTTCAAAAGTTAAATTTAAATTTCACTAATTGAACTAGT 2940
Qy 2941 GACAGAGAATGACATGATAGAGACTAAAGATCTAGCCCAATTTTATATTACTTG 3000
Db 2941 GACAGAGAATGACATGATAGAGACTAAAGATCTAGCCCAATTTTATATTACTTG 3000
Qy 3001 TTAGAAGATTTGAACAATTAATTAATTTCTTCAAGGTTCAATTTCCCATTAACATA 3060
Db 3001 TTAGAAGATTTGAACAATTAATTAATTTCTTCAAGGTTCAATTTCCCATTAACATA 3060
Qy 3061 ATGAATGTCTCATATTATGGGCGCTGAGAGAGCATTAATTAATTTGTAATTTGTAAT 3120
Db 3061 ATGAATGTCTCATATTATGGGCGCTGAGAGAGCATTAATTAATTTGTAATTTGTAAT 3120
Qy 3121 ATTGTATTAATTAATTAATTTGCTTTTAAATGATAGAGATTTTAAAGTATATG 3180
Db 3121 ATTGTATTAATTAATTAATTTGCTTTTAAATGATAGAGATTTTAAAGTATATG 3180

Qy 3181 TAACTGTAAACATAAAATGCAAAATGCCGTAAAGAGCAGTAGTAATAATATGATAT 3240
Db 3181 TAACTGTAAACATAAAATGCAAAATGCCGTAAAGAGCAGTAGTAATAATATGATAT 3240
Qy 3241 TATATTGTTATCATTAATCTAGCCTGTTTTTCCGTGTGTATTTCTTCTTAAATGCT 3300
Db 3241 TATATTGTTATCATTAATCTAGCCTGTTTTTCCGTGTGTATTTCTTCTTAAATGCT 3300
Qy 3301 TACAGAAATCTGTATCCCATTTCTTACCAACCAACCCCAACAATTTCTGCTTTTCCC 3360
Db 3301 TACAGAAATCTGTATCCCATTTCTTACCAACCAACCCCAACAATTTCTGCTTTTCCC 3360
Qy 3361 ATGCCGTCATGCTAACTTTGAAGCTTCAAGCTCTTCTCTCAATCTTCTCTGGC 3420
Db 3361 ATGCCGTCATGCTAACTTTGAAGCTTCAAGCTCTTCTCTCAATCTTCTCTGGC 3420
Qy 3421 ACCTCTGATATGCTTTTGAATTCATGTTAAAGAAATCCCTAGGCTGTATCAGATGG 3480
Db 3421 ACCTCTGATATGCTTTTGAATTCATGTTAAAGAAATCCCTAGGCTGTATCAGATGG 3480
Qy 3481 CATCTTTGTAGTACATGAATAATCAACTGTGTGTGTTTACGAAGATGATATGCTT 3540
Db 3481 CATCTTTGTAGTACATGAATAATCAACTGTGTGTGTTTACGAAGATGATATGCTT 3540
Qy 3541 CATTTGGGATTTGATTTTCTTCTTCTATCAGAGGAGAACTGAA 3586
Db 3541 CATTTGGGATTTGATTTTCTTCTTCTATCAGAGGAGAACTGAA 3586

RESULT 2
US-10-767-521-3
; Sequence 3, Application US/10767521
; Publication No. US20050033024A1
; GENERAL INFORMATION:
; APPLICANT: DAUGHERTY, BRUCE L.
; APPLICANT: DEMARTINO, JULIE A.
; APPLICANT: SICILIANO, SALVATORE J.
; APPLICANT: SPRINGER, MARTIN J.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING EOSINOPHIL EOTAXIN
; TITLE OF INVENTION: RECEPTOR
; FILE REFERENCE: 19634YDACA
; CURRENT APPLICATION NUMBER: US/10/767,521
; PRIOR FILING DATE: 2004-01-29
; PRIOR APPLICATION NUMBER: 60/016,158
; PRIOR FILING DATE: 1996-04-26
; PRIOR APPLICATION NUMBER: 09/922,895
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3586
; TYPE: DNA
; ORGANISM: Human
US-10-767-521-3

Query Match 100.0%; Score 3586; DB 8; Length 3586;
Best Local Similarity 100.0%; Pred. No; 0;
Matches 3586; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGAATCCCTACCTTCCCATCAGAGCTAGGCGCATGAGAGCGCTCTGCTAAGATGGGA 60
Db 1 GGAATCCCTACCTTCCCATCAGAGCTAGGCGCATGAGAGCGCTCTGCTAAGATGGGA 60
Qy 61 CCCCCAAGAAATGTCTCCCTGTGGGGCACTTCCTTACCAAGATGGGATGGCAGTGGGTT 120
Db 61 CCCCCAAGAAATGTCTCCCTGTGGGGCACTTCCTTACCAAGATGGGATGGCAGTGGGTT 120
Qy 121 AAGTTGTGTGTCAGGCAAGAAAAGATCTAAGTTGTACTTTGAGAGTTCCTGGGTTT 180
Db 121 AAGTTGTGTGTCAGGCAAGAAAAGATCTAAGTTGTACTTTGAGAGTTCCTGGGTTT 180
Qy 181 GTTCATGGCATGGGAGGAGTCAAGAGCAGCAGCGCTGCTCAAGTCCATCAGATGCA 240

Db 181 GTTCATGGCATGGGCAAGGAGTCAAGAGCAGCAGCCTTGCTCAGTGCCTACCAAGTGA 240
QY 241 GGAAGAAGTGATAGCCTGGGCGAGGGCCAGGGCCCTGGTGAAGCGTATGTTAAGAGA 300
Db 241 GGAAGAGGTGCATAGCCTGGGCGAGGGCCAGGGCCCTGGTGAAGCGTATGTTAAGAGA 300
QY 301 GAGGGCTCTCCATTCCAGGCCCAAGAGAAGCTAAGATGAATACCTCATGATATATTAGC 360
Db 301 GAGGGCTCTCCATTCCAGGCCCAAGAGAAGCTAAGATGAATACCTCATGATATATTAGC 360
QY 361 TACAAACCAACCAACAGCAGGTTCCAGAAAAGGCTCAGCGTTGGAAACCAAGTCACCCCCAG 420
Db 361 TACAAACCAACCAACAGCAGGTTCCAGAAAAGGCTCAGCGTTGGAAACCAAGTCACCCCCAG 420
QY 421 TCAGCAGACACCAAGTCATATTAATCAAGAGCAACACAGAGACAGAAACCCCCCTTCCCA 480
Db 421 TCAGCAGACACCAAGTCATATTAATCAAGAGCAACACAGAGACAGAAACCCCCCTTCCCA 480
QY 481 CTCTGCCCCATGTCTCAAGTTGTAGTGGCCCTTCTCCAGATCTCTGCCACCATCTTGA 540
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QY 541 AAGGAACACTGAAGAAGAACTGAATTTATTAAGCTGACAGCATTAAGAGGATGATGA 600
Db 541 AAGGAACACTGAAGAAGAACTGAATTTATTAAGCTGACAGCATTAAGAGGATGATGA 600
QY 601 ACCTAATAATCATTTGTTCACATGAATGAATCAAGAGAAGTTTAAACCACTTTGGACTTAAA 660
Db 601 ACCTAATAATCATTTGTTCACATGAATGAATCAAGAGAAGTTTAAACCACTTTGGACTTAAA 660
QY 661 TGTGTGAATCCTTTTCTCTGCTATCCAGCAGATGAGAAGCTGGTAAACAGAGACCAATTA 720
Db 661 TGTGTGAATCCTTTTCTCTGCTATCCAGCAGATGAGAAGCTGGTAAACAGAGACCAATTA 720
QY 721 GTTTGAGACTAAGAATCATTTGCACATTTCACTGCTGAGTTGTATTTGAGTAATTTTA 780
Db 721 GTTTGAGACTAAGAATCATTTGCACATTTCACTGCTGAGTTGTATTTGAGTAATTTTA 780
QY 781 GTTGAACCTCATTTTGTAAATCTTGACAACGGGGCAATCCAATATCTGACAAGAGATATG 840
Db 781 GTTGAACCTCATTTTGTAAATCTTGACAACGGGGCAATCCAATATCTGACAAGAGATATG 840
QY 841 TTAAACAGTGTAAATGCTGCATGAGAGATTGGGTGATTTTACTTTCTGTTTTGTGCT 900
Db 841 TTAAACAGTGTAAATGCTGCATGAGAGATTGGGTGATTTTACTTTCTGTTTTGTGCT 900
QY 901 CTTCTTTCTTATTTGTTCTTACTTATTTACGATTAACCTATCGTTTTCCCAAAATGTAAA 960
Db 901 CTTCTTTCTTATTTGTTCTTACTTATTTACGATTAACCTATCGTTTTCCCAAAATGTAAA 960
QY 961 GGGCAATTTGAAAAGCCTAATTCAAACTCTTCACTATTTTGTATCTAAGTATTCACCTTG 1020
Db 961 GGGCAATTTGAAAAGCCTAATTCAAACTCTTCACTATTTTGTATCTAAGTATTCACCTTG 1020
QY 1021 ATTGAAGCTGGGTAGACAGGTGAAGAAACCATATCAGGTTTAAATTTTAAATTTTAAAT 1080
Db 1021 ATTGAAGCTGGGTAGACAGGTGAAGAAACCATATCAGGTTTAAATTTTAAATTTTAAAT 1080
QY 1081 ATTATTTATTTATTTATTTTGTGAGATGAGTCTGGCTGCGCCAGCGCTGAGTGCAG 1140
Db 1081 ATTATTTATTTATTTATTTTGTGAGATGAGTCTGGCTGCGCCAGCGCTGAGTGCAG 1140
QY 1141 CGGCGGTGATCACAGTTCAGTGCAGCCTCAACCTTCTAGGCTCAAGGGAATCTCCCACTC 1200
Db 1141 CGGCGGTGATCACAGTTCAGTGCAGCCTCAACCTTCTAGGCTCAAGGGAATCTCCCACTC 1200
QY 1201 AGCCCCCAAGTAGTTGGACACACGTAATGCGCACCATGCTGCTAAATTTCTTATTT 1260
Db 1201 AGCCCCCAAGTAGTTGGACACACGTAATGCGCACCATGCTGCTAAATTTCTTATTT 1260
QY 1261 TTTTGTAGAGTAGGATCTACATATTTGTTCCAGGCTGTTGAATTCCTGGGCTCAGG 1320
Db 1261 TTTTGTAGAGTAGGATCTACATATTTGTTCCAGGCTGTTGAATTCCTGGGCTCAGG 1320

Db 1261 TTTTGTAGAGTAGGATCTACATATATTTGTTCCAGGCTGTTGAATTCCTGGGCTCAGG 1320
QY 1321 TGAACCTCCCACTGGGCTCCCAAAAGTACTGGGAATTAAGGCATGAGCCCAAGTCCCT 1380
Db 1321 TGAACCTCCCACTGGGCTCCCAAAAGTACTGGGAATTAAGGCATGAGCCCAAGTCCCT 1380
QY 1381 GCCCATATGAGATTTTCTGTCTCTGATCCCATGCACTAATCAAGGACTTGGCTGCT 1440
Db 1381 GCCCATATGAGATTTTCTGTCTCTGATCCCATGCACTAATCAAGGACTTGGCTGCT 1440
QY 1441 GACTCTGAGGACCTGCACTGCTTTCTTGAAGCTGTGAACCTCACTGCTAAAAGCTCATAGG 1500
Db 1441 GACTCTGAGGACCTGCACTGCTTTCTTGAAGCTGTGAACCTCACTGCTAAAAGCTCATAGG 1500
QY 1501 CAGCCTGAACCCCAACCAAAAGGTTCTATGTTTATCATCTGATCATGTGATTTTA 1560
Db 1501 CAGCCTGAACCCCAACCAAAAGGTTCTATGTTTATCATCTGATCATGTGATTTTA 1560
QY 1561 TAGAATAACACATGAATTAAGACACTACCTCAAACTGAGCAAAACTTAAGTAAATTTT 1620
Db 1561 TAGAATAACACATGAATTAAGACACTACCTCAAACTGAGCAAAACTTAAGTAAATTTT 1620
QY 1621 TTTAAAGTTTGACCTGTTTTTAAATCACTCTTTGGAGAAAAGAAAATAATACAATAA 1680
Db 1621 TTTAAAGTTTGACCTGTTTTTAAATCACTCTTTGGAGAAAAGAAAATAATACAATAA 1680
QY 1681 TTAAACGTTGAATACAGGCTTATACCTTTGTTCTCCAGAAATTAAGCAATCTGTTCTTTT 1740
Db 1681 TTAAACGTTGAATACAGGCTTATACCTTTGTTCTCCAGAAATTAAGCAATCTGTTCTTTT 1740
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Db 1741 CTTCCTTTAGATGCTGAAGTGAAGAGACACTCTGTGATTTGTAAGTGTAACTGACAA 1800
QY 1801 AATGTATTTTTTTTTCTGAGCTGCTATGATTTGAATTAAGTAAATGCAATGTC 1860
Db 1801 AATGTATTTTTTTTTCTGAGCTGCTATGATTTGAATTAAGTAAATGCAATGTC 1860
QY 1861 TGAATGGAGACACACAAACCAATTTGTTCTCAAGTCCATTTTCTCCTCAAAAGCCTGGA 1920
Db 1861 TGAATGGAGACACACAAACCAATTTGTTCTCAAGTCCATTTTCTCCTCAAAAGCCTGGA 1920
QY 1921 AATGTGCCATTGATCAGTGGGAGATGTACCTGACAGACCCATGAAGAGATCAACAAGT 1980
Db 1921 AATGTGCCATTGATCAGTGGGAGATGTACCTGACAGACCCATGAAGAGATCAACAAGT 1980
QY 1981 TCCACCCAAAGGACCCCTATTTTTCTTAATTCATTTGAATGAGCTCTAATTTGCTTCT 2040
Db 1981 TCCACCCAAAGGACCCCTATTTTTCTTAATTCATTTGAATGAGCTCTAATTTGCTTCT 2040
QY 2041 TTCAATCTGCTTCTTACCAAGTTTAAACAGCTTTTCTGCTTCAAAATGTGAACCTACATA 2100
Db 2041 TTCAATCTGCTTCTTACCAAGTTTAAACAGCTTTTCTGCTTCAAAATGTGAACCTACATA 2100
QY 2101 CACTCTCATTTTTCTCTCATCAACCCCAAGTGAACCAATGCTCTCACTTTCGATATTA 2160
Db 2101 CACTCTCATTTTTCTCTCATCAACCCCAAGTGAACCAATGCTCTCACTTTCGATATTA 2160
QY 2161 GTAAAGAGGCTCTGCAATTAAGGCTTGTCCAAAGGCAACGCACTGAGAGGCGCTAGACT 2220
Db 2161 GTAAAGAGGCTCTGCAATTAAGGCTTGTCCAAAGGCAACGCACTGAGAGGCGCTAGACT 2220
QY 2221 GGGTCATTTCCATCTATTTCTCACTGACTTTGACTTACCAAGAACCCCAACATGTGGGG 2280
Db 2221 GGGTCATTTCCATCTATTTCTCACTGACTTTGACTTACCAAGAACCCCAACATGTGGGG 2280
QY 2281 CCTCAGTATTCGATCAATTAATTTATTAAGAGCAAAAACAATCCCGCATTTGGCCCCA 2340
Db 2281 CCTCAGTATTCGATCAATTAATTTATTAAGAGCAAAAACAATCCCGCATTTGGCCCCA 2340
QY 2341 GTTATTAAGCAATTTCTCAGATTTACCTTGAGAAATGCCCATGCGCTGTATATTCACATC 2400
Db 2341 GTTATTAAGCAATTTCTCAGATTTACCTTGAGAAATGCCCATGCGCTGTATATTCACATC 2400

QY 2401 TTCACTTGTGCCCTTCTCCTAGAAAAGAGAAAGTCAAGTGAATGCCCTCTGAGAACT 2460
DB 2401 TTCACTTGTGCCCTTCTCCTAGAAAAGAGAAAGTCAAGTGAATGCCCTCTGAGAACT 2460
QY 2461 AGTGCATGGCTTAACTGTCTTCCATGACTCTCTGCTTATCTGTTTCTATTCTCTCT 2520
DB 2461 AGTGCATGGCTTAACTGTCTTCCATGACTCTCTGCTTATCTGTTTCTATTCTCTCT 2520
QY 2521 TTTCACCCGAAGTCTATATCTCAAGAAAAGCAGGCACTGGCCTTAGGGCTCTGGCCTA 2580
DB 2521 TTTCACCCGAAGTCTATATCTCAAGAAAAGCAGGCACTGGCCTTAGGGCTCTGGCCTA 2580
QY 2581 AGAAATATCAAGTCCAGTGAAGAAATCCCATTTGACTGACCCCTGCTTACCCCTTTGTG 2640
DB 2581 AGAAATATCAAGTCCAGTGAAGAAATCCCATTTGACTGACCCCTGCTTACCCCTTTGTG 2640
QY 2641 ATGAGAAAGCTCCAGGGGTTTGTCTTTTGCATGTACCAAGGCTTAATCTCAGCATCACA 2700
DB 2641 ATGAGAAAGCTCCAGGGGTTTGTCTTTTGCATGTACCAAGGCTTAATCTCAGCATCACA 2700
QY 2701 GGGGCAAGAAAAGGAAAGTAACTAACTAATGCTGCTTATATTTGTAATTTATGTAATA 2760
DB 2701 GGGGCAAGAAAAGGAAAGTAACTAACTAATGCTGCTTATATTTGTAATTTATGTAATA 2760
QY 2761 GTTAATTAATCTGTGATTTGATGATGTAAGACAGACAAATGTAATTTTTCACAGCTGCT 2820
DB 2761 GTTAATTAATCTGTGATTTGATGATGTAAGACAGACAAATGTAATTTTTCACAGCTGCT 2820
QY 2821 GTGATTTGATTTATGCAATTTTGAATTAAGAAATGCTGTTAAGAGCACAAAGCAGGTTCC 2880
DB 2821 GTGATTTGATTTATGCAATTTTGAATTAAGAAATGCTGTTAAGAGCACAAAGCAGGTTCC 2880
QY 2881 TCAGTCCGTAGCAAAATTTTCAAAAGTTAAATTTAAATCACTAATTTGAATCTAGT 2940
DB 2881 TCAGTCCGTAGCAAAATTTTCAAAAGTTAAATTTAAATCACTAATTTGAATCTAGT 2940
QY 2941 GACAGAGAAATGACATGATAGAGCTAAAGATCTAGCCCAATTTTATATTACTTCTG 3000
DB 2941 GACAGAGAAATGACATGATAGAGCTAAAGATCTAGCCCAATTTTATATTACTTCTG 3000
QY 3001 TTAGAGATTTTGAACAAATTTCTTCAAGGTTCAATTTCCCATTAATATA 3060
DB 3001 TTAGAGATTTTGAACAAATTTCTTCAAGGTTCAATTTCCCATTAATATA 3060
QY 3061 ATGAATGCTCATCATATATGAGGCTGAGAGAGAGATTAATTTGTAATGTAATATC 3120
DB 3061 ATGAATGCTCATCATATATGAGGCTGAGAGAGAGATTAATTTGTAATGTAATATC 3120
QY 3121 ATTGTAATTAATTAATATATATTTCTTTTAAATGATAGATTTTAAAGTATATG 3180
DB 3121 ATTGTAATTAATTAATATATATTTCTTTTAAATGATAGATTTTAAAGTATATG 3180
QY 3181 TAAACTGTAAACATTAATATGCAAAATGCCGTAAGAGACAGTAAATTAATGATTAAT 3240
DB 3181 TAAACTGTAAACATTAATATGCAAAATGCCGTAAGAGACAGTAAATTAATGATTAAT 3240
QY 3241 TATAATGTAATCATTAATCTAGGCTGTTTCTGTTGTAATTTCTCTTAAATGCT 3300
DB 3241 TATAATGTAATCATTAATCTAGGCTGTTTCTGTTGTAATTTCTCTTAAATGCT 3300
QY 3301 TACAGAAATCTGTATCCCATTTCTCAACCAACCCACAAATTTCTGCTTTTCCC 3360
DB 3301 TACAGAAATCTGTATCCCATTTCTCAACCAACCCACAAATTTCTGCTTTTCCC 3360
QY 3361 ATGCCGTCATGCTAACTTTGAAGCTTCAAGCTTTCTCTCAATCTCTCTGCTG 3420
DB 3361 ATGCCGTCATGCTAACTTTGAAGCTTCAAGCTTTCTCTCAATCTCTCTGCTGCTG 3420
QY 3421 ACCTGTATATGCTTTTGAATTTCAATGTTAAAGATCCCTAGGCTGCTATCAGATGTGG 3480
DB 3421 ACCTGTATATGCTTTTGAATTTCAATGTTAAAGATCCCTAGGCTGCTATCAGATGTGG 3480

QY 3481 CATCTTTGTGAGTACATGAATTAATCAACTGTGTGTTTACGAAGATGATTAATGCTT 3540
DB 3481 CATCTTTGTGAGTACATGAATTAATCAACTGTGTGTTTACGAAGATGATTAATGCTT 3540
QY 3541 CATGTGGGATTTGATTTTCTTCTTCTATCAGAGGAGAGTGA 3586
DB 3541 CATGTGGGATTTGATTTTCTTCTTCTATCAGAGGAGAGTGA 3586

RESULT 3
US-10-929-182-21
; Sequence 21, Application US/10929182
; Publication No. US20050064483A1
; GENERAL INFORMATION:
; APPLICANT: Zang, Jingwu
; APPLICANT: Hong, Jian
; TITLE OF INVENTION: Gene Expression Profiling Technology for Treatment Evaluation of
; FILE REFERENCE: HO-P02859US1
; CURRENT APPLICATION NUMBER: US/10/929,182
; PRIOR FILING DATE: 2004-08-30
; PRIOR APPLICATION NUMBER: US 60/498,731
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 21
; LENGTH: 5791
; TYPE: DNA
; ORGANISM: HUMAN
US-10-929-182-21

Query Match 97.4%; Score 3494.4; DB 9; Length 5791;
Best Local Similarity 99.5%; Pred. No. 10;
Matches 3569; Conservative 0; Mismatches 11; Indels 8; Gaps 6;

QY 1 GGATCCCTAACCTTCCCATCAAGCTAGGGGGCATGAGCGCTCTGCTAAGATGGGA 60
DB 433 GGATCCCTAACCTTCCCATCAAGCTAGGGGGCATGAGCGCTCTGCTAAGATGGGA 492
QY 61 CCCCAGGAATGTCTCCCTGTGGGGCACTTCTTACCAAGATGGGATGGCAGTGGGTT 120
DB 493 CCCCAGGAATGTCTCCCTGTGGGGCACTTCTTACCAAGATGGGATGGCAGTGGGTT 552
QY 121 AAGTTGGTGTGAGGAGGAGAAAGATGATTTGTAATCTGAGAGTTCTCGGTTT 180
DB 553 AAGTTGGTGTGAGGAGGAGGAGAAAGATGATTTGTAATCTGAGAGTTCTCGGTTT 612
QY 181 GTTCATGGCATGGGAGGAGTCAAGAGCAGCAGCTTGGCTCAAGTCCCTACCAAGTGA 240
DB 613 GTTCATGGCATGGGAGGAGTCAAGAGCAGCAGCTTGGCTCAAGTCCCTACCAAGTGA 672
QY 241 GGAAGAGTGCATAGCTGGGCGAGGGCCAGGGCCCTGTTGAGGCGTAGTGTAACAGA 300
DB 673 GGAAGAGTGCATAGCTGGGCGAGGGCCAGGGCCCTGTTGAGGCGTAGTGTAACAGA 732
QY 301 GAGGCTCTCCATTCCAGCCCAAGAGAGCTAAGATGAATACCTCATGATATATTAGC 360
DB 733 GAGGCTCTCCATTCCAGCCCAAGAGAGCTAAGATGAATACCTCATGATATATTAGC 792
QY 361 TACAAACCAACACAGCAGGTTCCAGAAAAGGCTCAGCGTTGGAACAGGTCAACCCCTTCCA 420
DB 793 TACAAACCAACACAGCAGGTTCCAGAAAAGGCTCAGCGTTGGAACAGGTCAACCCCTTCCA 852
QY 421 TCAGCAGACACAGTCAATATAATCAAGAGCACAAGAGAGAGAGAGAGAGAGAGAGAGAG 480
DB 853 TCAGCAGACACAGTCAATATAATCAAGAGCACAAGAGAGAGAGAGAGAGAGAGAGAGAG 912
QY 481 CTGTGCCCATGTCTCAAGTTGTAAGTGGCCCTTCTCCAGATCTGTGCCACCATCTTGA 540
DB 913 CTGTGCCCATGTCTCAAGTTGTAAGTGGCCCTTCTCCAGATCTGTGCCACCATCTTGA 972
QY 541 AAGGAACACTGAAGAGAGAACTGAATTAATTAAGCTGACAGATAAAGAGATGATTA 600

Db 973 AAGGAACACTGAAAAGAGAACTGAAATTATTAAGCTGACAGCATTAAGAGGATGAGTAA 1032
Qy 601 ACCTAAATCATTTGTTCACATGAAATGAAATCAAGAGAAGTTTAAACCACTTGGACTTAAA 660
Db 1033 ACCTAAATCAITGTTTCAAAATGAATGAATCAAGAGAAGTTTAAACCACTTGGACTTAAA 1092
Qy 661 TGTGTGAATCCTTTTCCGTGCTATCCAGCATGAGAAGCTGGTAAACAGAGACCACATTA 720
Db 1093 TGTGTGAATCCTTTTCCGTGCTATCCAGCATGAGAAGCTGGTAAACAGAGACCACATTA 1152
Qy 721 GTTTGAGACTTAAAGAAATCATGTCACATTTCACTGCTGAGTTGTATTTGTGAGTAATTTA 780
Db 1153 GTTTGAGACTTAAAGAAATCATGTCACATTTCACTGCTGAGTTGTATTTGTGAGTAATTTA 1212
Qy 781 GTTGAACCTCAC-TTTGTAATCTTGCAACGGGGCAATCCAATATCTGCAACAAGATAT 839
Db 1213 GTTGAACCTCAC-TTTGTAATCTTGCAACGGG---CATCCATATCTGCAAC-AGAGATAT 1268
Qy 840 GTTAAACAGTGTGAATATGCTGCATGAGAGATTTGGGTGATTTTAACTTTCGTTTGTGC 899
Db 1269 GTTAA-CAGTGTGAATATGCTGCATGAGAGATTTGGGTGATTTTAACTTTCGTTTGTGC 1327
Qy 900 TCTTCTTTCTTATTTGTCTTACTATTTTAAACGATTAACCTATCGTTTCCCAAAATGTAA 959
Db 1328 TCTTCTTTCTTATTTGTCTTACTATTTTAAACGATTAACCTATCGTTT-CCAAATGTAA 1386
Qy 960 AGGCCATTTTGAAGCCCTAATTCAAACCTCTTCACTATTTTGTATCTAAGTATTCACCTT 1019
Db 1387 AGGCCATTTTGAAGCCCTAATTCAAACCTCTTCACTATTTTGTATCTAAGTATTCACCTT 1446
Qy 1020 GATTGAGACTGGGTAGACAGGTGAAGAAACATATCAGGTTTAAATTTTAAATTTTAAAT 1079
Db 1447 GATTGAGACTGGGTAGACAGGTGAAGAAACATATCAGGTTTAAATTTTAAATTTTAAAT 1506
Qy 1080 TATTTATTTATTTATTTATTTTGTAGATGAGTCTGGCTGTGCCCCAGGCTGAGTGCA 1139
Db 1507 TATTTATTTATTTATTTATTTTGTAGATGAGTCTGGCTGTGCCCCAGGCTGAGTGCA 1566
Qy 1140 GCGGCGTGATTCACAGTTCAGTTCAGGCTCAACCTTCTAGGCTCAAGGGAATCTCCACCT 1199
Db 1567 GCGGCGTGATTCACAGTTCAGTTCAGGCTCAACCTTCTAGGCTCAAGGGAATCTCCACCT 1626
Qy 1200 CAGCCCCCAAGTAGTGTGGACCACACGTAATGCGCCACCATGCTGCTAATTTCTTAT 1259
Db 1627 CAGCCCCCAAGTAGTGTGGACCACACGTAATGCGCCACCATGCTGCTAATTTCTTAT 1686
Qy 1260 TTTTGTGAGATAGGATCTCACTATATTTGTCAGGCTGCTGTAATTCCTGGGCTCAG 1319
Db 1687 TTTTGTGAGATAGGATCTCACTATATTTGTCAGGCTGCTGTAATTCCTGGGCTCAG 1746
Qy 1320 GTGAGCCTCCCACTGGGCTCCCAAAAGTACTGGGATTAACAGCATGAGCCAAAGTCCCC 1379
Db 1747 GTGAGCCTCCCACTGGGCTCCCAAAAGTACTGGGATTAACAGCATGAGCCAAAGTCCCC 1806
Qy 1380 TGCCCATATGAGATTTTCTGTCTGTGATCCCATGCACTAGTATCAAGGACTTGGCTGC 1439
Db 1807 TGCCCATATGAGATTTTCTGTCTGTGATCCCATGCACTAGTATCAAGGACTTGGCTGC 1866
Qy 1440 TGACTCTGAGGACTGTCATGCTTCTTGAGCTGTGAACCTCAGTGTAAAGCTCATAG 1499
Db 1867 TGACTCTGAGGACTGTCATGCTTCTTGAGCTGTGAACCTCAGTGTAAAGCTCATAG 1926
Qy 1500 GCAGCCCTGAAACCCAAACCAAAAGTTCTATGTTTATCATCCTGATCATGTTGATTTT 1559
Db 1927 GCAGCCCTGAAACCCAAACCAAAAGTTCTATGTTTATCATCCTGATCATGTTGATTTT 1986
Qy 1560 ATAGAATAAACAATGAATTAAGAACAACCTCAAACTGAGCAAAACCTTAAGTAATTT 1619
Db 1987 ATAGAATAAACAATGAATTAAGAACAACCTCAAACTGAGCAAAACCTTAAGTAATTT 2046
Qy 1620 TTTTAAAGTTGACCTGTTTAAATCACTCTTGAGAGAAAAAGGAAATTAATAATAATA 1679
Db 2047 TTTTAAAGTTGACCTGTTTAAATCACTCTTGAGAGAAAAAGGAAATTAATAATAATA 2106

Qy 1680 ATTTAACGGTGAATACAGGCTACTATACCTTTGTTCTCCAGAAATTAAGAGTTCTGTTCTTT 1739
Db 2107 ATTTAACGGTGAATACAGGCTACTATACCTTTGTTCTCCAGAAATTAAGAGTTCTGTTCTTT 2166
Qy 1740 TCTTGCTTTAGATGCTGAAGTGCAGAAGGACACTCTGTGATTTGTACGTGTGTACTGACA 1799
Db 2167 TCTTGCTTTAGATGCTGAAGTGCAGAAGGACACTCTGTGATTTGTACGTGTGTACTGACA 2226
Qy 1800 AAATGTATTTTATTTTCTCAGCTGCTATGATTTGAATTAATGCTATTAATGAATAAGATG 1859
Db 2227 AAATGTATTTTATTTTCTCAGCTGCTATGATTTGAATTAATGCTATTAATGAATAAGATG 2286
Qy 1860 CTGAATGGAGACACACAAACCAATTTGTTCTCAGTCCATTTTCTCCTCAAAAGCCTGG 1919
Db 2287 CTGAATGGAGACACACAAACCAATTTGTTCTCAGTCCATTTTCTCCTCAAAAGCCTGG 2346
Qy 1920 AATGTCCATTGATCAGTGGAGATGTACCTGACAGACCAATGAAGAAAGATCAACAAG 1979
Db 2347 AATGTCCATTGATCAGTGGAGATGTACCTGACAGACCAATGAAGAAAGATCAACAAG 2406
Qy 1980 TTCCACCCCAAGGAGCCCATTTTCTCTAATTTCAATTTGAATGCGCTCTAATGTCTTC 2039
Db 2407 TTCCACCCCAAGGAGCCCATTTTCTCTAATTTCAATTTGAATGCGCTCTAATGTCTTC 2466
Qy 2040 TTTCAATCTGCTCTTCTTACAGATTTTACAGCTTTTCTGCTTCAATGTGAATCTCAAT 2099
Db 2467 TTTCAATCTGCTCTTCTTACAGATTTTACAGCTTTTCTGCTTCAATGTGAATCTCAAT 2526
Qy 2100 ACACCTCATTTTCTCTCATCAACAACCCCAAGTGACCCCAATGCTCTCATTTGATATA 2159
Db 2527 ACACCTCATTTTCTCTCATCAACAACCCCAAGTGACCCCAATGCTCTCATTTGATATA 2586
Qy 2160 AGTAAGAGAGGCTCTGCATTAAGGCTGTGCCAAGGACGCACTGAGAGCGCTAGGAC 2219
Db 2587 AGTAAGAGAGGCTCTGCATTAAGGCTGTGCCAAGGACGCACTGAGAGCGCTAGGAC 2646
Qy 2220 TGGCTTCATTTCCATCTCTATTTCTCACTGACTTTGACTTACCAACCCCAATGTGG 2279
Db 2647 TGGCTTCATTTCCATCTCTATTTCTCACTGACTTTGACTTACCAACCCCAATGTGG 2706
Qy 2280 GCGTCAATTCGATCAATTAATTTCTATTAAGAGCAAAACAATTCGCCCATTTGGCCCC 2339
Db 2707 GCGTCAATTCGATCAATTAATTTCTATTAAGAGCAAAACAATTCGCCCATTTGGCCCC 2766
Qy 2340 AGTTAATAAGCATTTCTCAGATTTACCTTGAAGAAATGCCATGCGCTGTATATTACAT 2399
Db 2767 AGTTAATAAGCATTTCTCAGATTTACCTTGAAGAAATGCCATGCGCTGTATATTACAT 2826
Qy 2400 CTTCAACCTTGTCCCTTCTCCTCCTAAGAAAGAGAAAGTCAATGGAATGCCCTGAGGAAC 2459
Db 2827 CTTCAACCTTGTCCCTTCTCCTCCTAAGAAAGAGAAAGTCAATGGAATGCCCTGAGGAAC 2886
Qy 2460 TAGTGATGGCTTAACCTGTCTTCATGACTCTGCTTATCTGTTTCTATTTTCTCTCC 2519
Db 2887 TAGTGATGGCTTAACCTGTCTTCATGACTCTGCTTATCTGTTTCTATTTTCTCTCC 2946
Qy 2520 TTTTCCACCGAAGTCTATATCTCAAGAAAGCAGGCACTGGCCTTAAGGGCTCCTGGCCT 2579
Db 2947 TTTTCCACCGAAGTCTATATCTCAAGAAAGCAGGCACTGGCCTTAAGGGCTCCTGGCCT 3006
Qy 2580 AAGAATAATCAAGTCCAGTGAGAAATCCCAATGACTGACCCCTCTGCTTAACCCCTTGT 2639
Db 3007 AAGAATAATCAAGTCCAGTGAGAAATCCCAATGACTGACCCCTCTGCTTAACCCCTTGT 3066
Qy 2640 GATGAGAGAGCTCCCAAGGGGTTGCTTTTGTGATGTACCAAGGCTTAACCATCACCC 2699
Db 3067 GATGAGAGAGCTCCCAAGGGGTTGCTTTTGTGATGTACCAAGGCTTAACCATCACCC 3126
Qy 2700 AGGGGCAAGAAAGGAAAGTAACCTTAACCTAATGCTGCTTATTAATTTGTAAT 2759
Db 3127 AGGGGCAAGAAAGGAAAGTAACCTTAACCTAATGCTGCTTATTAATTTGTAAT 3186


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OY 2760 AGTTAATTACTGTGATTGTACATGTGTACACAGACAAATGTGTAATTTTTCACAGCTGC 2819
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DB 3187 AGTTAATTACTGTGATTGTACATGTGTAAACAGACAAATGTGTAATTTTTCACAGCTGC 3246
OY 2820 TGTGATTGATTATGCAATTTGGAATTAAGAAATGCTGTTAAGACACACAGCCAGTTC 2879
      |||||||
DB 3247 TGTGATTGATTATGCAATTTGGAATTAAGAAATGCTGTTAAGACACACAGCCAGTTC 3306
OY 2880 CTCAAGTCCGTAGCAAAATTTTCAAAAGTTAAATTTAAATCACTACATTTGAATCTAG 2939
      |||||||
DB 3307 CTCAAGTCCGTAGCAAAATTTTCAAAAGTTAAATTTAAATCACTACATTTGAATCTAG 3366
OY 2940 TGACAGAGAAATGACATGAGATAGAGACTAAAGATCTAGCCCAATTTTATATTTACTT 2999
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DB 3367 TGACAGAGAAATGACATGAGATAGAGACTAAAGATCTAGCCCAATTTTATATTTACTT 3426
OY 3000 GTTAAAGGATTTTGAACAAATTACTAAATTTCTCAAGGTTCAATTTCCCATTAATCTAT 3059
      |||||||
DB 3427 GTTAAAGGATTTTGAACAAATTACTAAATTTCTCAAGGTTCAATTTCCCATTAATCTAT 3486
OY 3060 AATGAATGTCCTCATCTATATGAGGCGCTGAGAGACATAATTACTGTAAATGTAAATAT 3119
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DB 3487 AATGAATGTCCTCATCTATATGAGGCGCTGAGAGACATAATTACTGTAAATGTAAATAT 3546
OY 3120 CATGTTATATATATATATATATATTTGCTTTTAAATGATAAGATTTTAAAGGTAAT 3179
      |||||||
DB 3547 CATGTTATATATATATATATATATTTGCTTTTAAATGATAAGATTTTAAAGGTAAT 3606
OY 3180 GTAAACTGTAAACATAAATGCAAAATGCCGTAAAGACAGTAATATAATATGATTA 3239
      |||||||
DB 3607 GTAAACTGTAAACATAAATGCAAAATGCCGTAAAGACAGTAATATAATATGATTA 3666
OY 3240 TTATATGTTATCATATATAGCTGTTTTTCTGTTGTTGTAATTTCTTCTTAAATGC 3299
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DB 3667 TTATATGTTATCATATATAGCTGTTTTTCTGTTGTTGTAATTTCTTCTTAAATGC 3726
OY 3300 TTACAGAAATCTGATATCCCAATCTTCAACCAACCCCAACAATTTCTGCTTCTTCC 3359
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DB 3727 TTTCAGAAATCTGATATCCCAATCTTCAACCAACCCCAACAATTTCTGCTTCTTCC 3786
OY 3360 CATGCC-GGTCAATGTAATTTGAAGCTTCAGCTCTTCTCTCAATCTTCTCTG 3418
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DB 3787 CATGCCGGGTCAATGTAATTTGAAGCTTCAGCTCTTCTCTCAATCTTCTCTG 3846
OY 3419 GCACTCTGATATGCTTTTGAATTTCAATGTTAAAGAAATCCCTAGGCTGCTATCAATGT 3478
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DB 3847 GCACTCTGATATGCTTTTGAATTTCAATGTTAAAGAAATCCCTAGGCTGCTATCAATGT 3906
OY 3479 GGCATCTTGTGATGATGATGAATCAACTGCTGTTTGAAGAGATGATATGC 3538
      |||||||
DB 3907 GGCATCTTGTGATGATGATGAATCAACTGCTGTTTGAAGAGATGATATGC 3966
OY 3539 TTCAATGTGGATGTAATTTTCTTCTCTATCACAGGAGAGATGAA 3586
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DB 3967 TTCAATGTGGATGTAATTTTCTTCTCTATCACAGGAGAGATGAA 4014

RESULT 4
US-10-486-471-5
; Sequence 5, Application US/10486471
; Publication No. US20050101530A1
; GENERAL INFORMATION:
; APPLICANT: TOPIGEN PHARMACEUTIQUE INC.
; TITLE OF INVENTION: CELLULAR VIRUS RECEPTORS AND METHODS OF USE
; FILE REFERENCE: 009553-0003
; CURRENT APPLICATION NUMBER: US/10/486,471
; PRIOR FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: U.S. 60/311,088
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 5791
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      TYPE: DNA
      ORGANISM: Homo sapiens
      FEATURE:
      NAME/KEY: CDS
      LOCATION: (4015)..(5082)
      OTHER INFORMATION:
      PUBLICATION INFORMATION:
      DATABASE ACCESSION NUMBER: GenBank AF247361
      DATABASE ENTRY DATE: 2002-06-26
      RELEVANT RESIDUES: (1)..(5791)
US-10-486-471-5

Query Match          97.4%; Score 3494.4; DB 9; Length 5791;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 3569; Conservative 0; Mismatches 11; Indels 8; Gaps 6;

OY 1 GGAATCCCTACCTTCCCATACAGCTAAGGGGCGATGAGCGCTCTCTGTAAGATGGGA 60
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DB 433 GGAATCCCTACCTTCCCATACAGCTAAGGGGCGATGAGCGCTCTCTGTAAGATGGGA 492
OY 61 CCCCCAAGAAATGTCCTCCTGTGGGGCACTTCTTACAGATGGGATGGCAATGCGGTT 120
      |||||||
DB 493 CCCCCAAGAAATGTCCTCCTGTGGGGCACTTCTTACAGATGGGATGGCAATGCGGTT 552
OY 121 AAGTGTGTGTCAGGCAAGAAAAAAGATCTAGTTTGTACTCTGAGAGTTCCTCGGTTT 180
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DB 553 AAGTGTGTGTCAGGCAAGAAAAAAGATCTAGTTTGTACTCTGAGAGTTCCTCGGTTT 612
OY 181 GTTCATGGCATGGGCAAGAGTCAAGAGCAGACGCTGCTCAAGTCCCTACCAATGCA 240
      |||||||
DB 613 GTTCATGGCATGGGCAAGAGTCAAGAGCAGACGCTGCTCAAGTCCCTACCAATGCA 672
OY 241 GGAAGAGGTGCATAGCCTGCGGCCAGGGCCCTGTGGAGGCGGTAGTGTAAACAGA 300
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DB 673 GGAAGAGGTGCATAGCCTGCGGCCAGGGCCCTGTGGAGGCGGTAGTGTAAACAGA 732
OY 301 GAGGCTCTCCATTCAGGCCAAGGAAGCTAAGAAATGAATTAATCTCATGATATATAGC 360
      |||||||
DB 733 GAGGCTCTCCATTCAGGCCAAGGAAGCTAAGAAATGAATTAATCTCATGATATATAGC 792
OY 361 TACAACCAACCAAGCAGGTTCCAGAAAAAGGCTCAGCGTTGGAACCAAGTCAACCCCA 420
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DB 793 TACAACCAACCAAGCAGGTTCCAGAAAAAGGCTCAGCGTTGGAACCAAGTCAACCCCA 852
OY 421 TCAGCAGACACCAAGTCAATTAATCAAGAACCAACAGAGACAGGAACACCCCTCCCA 480
      |||||||
DB 853 TCAGCAGACACCAAGTCAATTAATCAAGAACCAACAGAGACAGGAACACCCCTCCCA 912
OY 481 CTCGCCCCATGTCTCAAGTTGTAAGTGGCCCTTCTCTCAGATCTCTGCCACCATCTTGA 540
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DB 913 CTCGCCCCATGTCTCAAGTTGTAAGTGGCCCTTCTCTCAGATCTCTGCCACCATCTTGA 972
OY 541 AAGGAACACTGAAGAGAACTGAATTTTAAGCTGACAGCATTAAGAGATGATGAAA 600
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DB 973 AAGGAACACTGAAGAGAACTGAATTTTAAGCTGACAGCATTAAGAGATGATGAAA 1032
OY 601 ACCTAAATCATTTGTTCAATGAATGAATCAAGAGAGTTTAAACCACTTGAAGTAAA 660
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DB 1033 ACCTAAATCATTTGTTCAATGAATGAATCAAGAGAGTTTAAACCACTTGAAGTAAA 1092
OY 661 TGTGTGAATCTTTTCTGCTATCCAGAGATGAGAGCTGTAAACAGAGACCAATA 720
      |||||||
DB 1093 TGTGTGAATCTTTTCTGCTATCCAGAGATGAGAGCTGTAAACAGAGACCAATA 1152
OY 721 GTTTGAGACTAAAGATCATTTGCAATTTCACTGCTGAGTTGTAATTTGTAATTTTA 780
      |||||||
DB 1153 GTTTGAGACTAAAGATCATTTGCAATTTCACTGCTGAGTTGTAATTTGTAATTTTA 1212
OY 781 GTTGACCTCAC-TTGTAAATCTTGACACAGGGGCAATCCAATATCTGCACAAGAGATAT 839
      |||||||
DB 1213 GTTGACCTCAC-TTGTAAATCTTGACACAGGGG--CATCCATATCTGCAC-AGAGATAT 1268
OY 840 GTTAAACAGTGTAAATGCTGATGAGAGATTTGGTGAATTTTACTTTTCGTTTGTGTC 899
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Db 1269 GTTAA-CAGTGTAAATGCTGACGAGAGATTGGGTGATTTTAACTTTCGTTTTCGTC 1327
QY 900 TCTTCTTCTTATTTGTTCTTACTTAATTACGATTACCCTTACGTTTCCCAAAATGTAA 959
Db 1328 TCTTCTTCTTATTTGTTCTTACTTAATTACGATTACCCTATCGTTT-CCAAATGTAA 1386
QY 960 AGGCCATTTTGAAGCCTAATTCAAACCTTCACTATTTTGTATCTAAGTATTCACCT 1019
Db 1387 AGGCCATTTTGAAGCCTAATTCAAACCTTCACTATTTTGTATCTAAGTATTCACCT 1446
QY 1020 GATTGAGACTGGGTAGACAGGTGAAACCATATCAGGTTTTHAATTTTTHAATTTTHAAT 1079
Db 1447 GATTGAGACTGGGTAGACAGGTGAAACCATATCAGGTTTTHAATTTTTHAATTTTTHAAT 1506
QY 1080 TATTATTTATTTATTTATTTTGGAGTGGTCTGCTGCTGCCAGGCTGAGTGCA 1139
Db 1507 TATTATTTATTTATTTATTTTGGAGTGGTCTGCTGCTGCCAGGCTGAGTGCA 1566
QY 1140 GCGGCGTATCAAGTTCACTGACGCTCAACCTTCTAGGCTCAAGGATTCTCCACCT 1199
Db 1567 GCGGCGTATCAAGTTCACTGACGCTCAACCTTCTAGGCTCAAGGATTCTCCACCT 1626
QY 1200 CAGCCCCCAAGTAGTTGGACCAAGATGCGCCACCATGCGCTAATTTCTAT 1259
Db 1627 CAGCCCCCAAGTAGTTGGACCAAGATGCGCCACCATGCGCTAATTTCTAT 1686
QY 1260 TTTTGTAGAGATAGGATCTCACTATATTTGTCCAGGCTGCTTGAATTCCTGGGCTAG 1319
Db 1687 TTTTGTAGAGATAGGATCTCACTATATTTGTCCAGGCTGCTTGAATTCCTGGGCTAG 1746
QY 1320 GTGAGCTCCCACTGCGGCTCCCAAGTACTGGGATTACAGGCAAGCCAAAGTCCCC 1379
Db 1747 GTGAGCTCCCACTGCGGCTCCCAAGTACTGGGATTACAGGCAAGCCAAAGTCCCC 1806
QY 1380 TGGCCATATAGATTTTCTGCTCTGATCCCATGACGCTAGTATCAAGGACTTGCGTGC 1439
Db 1807 TGGCCATATAGATTTTCTGCTCTGATCCCATGACGCTAGTATCAAGGACTTGCGTGC 1866
QY 1440 TGACTGTGAGGAGCTGACGCTTTCTTGAGCTGTGAACCTTCAAGTCTAAAGCTCATAG 1499
Db 1867 TGACTGTGAGGAGCTGACGCTTTCTTGAGCTGTGAACCTTCAAGTCTAAAGCTCATAG 1926
QY 1500 GCAGCCCTGAAAACCCAAACCAAAAGGTTCTATGCTTTATCATCTGATCATGTGATTTT 1559
Db 1927 GCAGCCCTGAAAACCCAAACCAAAAGGTTCTATGCTTTATCATCTGATCATGTGATTTT 1986
QY 1560 ATAGAATAACACATGAATTAAAGACACTAACCTCAAACTGAGCAAACTTAAGTAAAT 1619
Db 1987 ATAGAATAACACATGAATTAAAGACACTAACCTCAAACTGAGCAAACTTAAGTAAAT 2046
QY 1620 TTTTAAAGTTGACCTGTTTTTAAATCACTGTGAGAAAAAGAAAAATAAATACAATA 1679
Db 2047 TTTTAAAGTTGACCTGTTTTTAAATCACTGTGAGAAAAAGAAAAATAAATACAATA 2106
QY 1680 ATTAACGGTGAATACAGGCTACTATACCTTGTCTCCAGAATTAGCAGTTCTGTTCTTT 1739
Db 2107 ATTAACGGTGAATACAGGCTACTATACCTTGTCTCCAGAATTAGCAGTTCTGTTCTTT 2166
QY 1740 TCTTGCCTTAAGTCTGAAGTGCAAGAGACACTCTGTGATTTGTACGTTGTAACTGACA 1799
Db 2167 TCTTGCCTTAAGTCTGAAGTGCAAGAGACACTCTGTGATTTGTACGTTGTAACTGACA 2226
QY 1800 AAATGTGTATTTTTTCTCAGCTGCTATGGAATTGGAATTATGCTATTAAGATAAGATG 1859
Db 2227 AAATGTGTATTTTTTCTCAGCTGCTATGGAATTGGAATTATGCTATTAAGATAAGATG 2286
QY 1860 CTGATGGAGACACACAACCATTTGTTCTCAGTCCATTTTCTCTCAAAAAGCCTGG 1919
Db 2287 CTGATGGAGACACACAACCATTTGTTCTCAGTCCATTTTCTCTCAAAAAGCCTGG 2346
QY 1920 AATGTGCCATTGATCAGTGGAGATGTACCTGACAGCCCATGAAAAGAGATCAACAAG 1979

Db 2347 AATGTGCCATTGATCAGTGGAGATGTACCTGAGACAGCCATGAAAAGAGATCAACAAG 2406
QY 1980 TTCCACCCCAAGGAGCCCTAATTTTCTCTAATTTCAATTGAATGCGCTTCTAATTGCTTC 2039
Db 2407 TTCCACCCCAAGGAGCCCTAATTTTCTCTAATTTCAATTGAATGCGCTTCTAATTGCTTC 2466
QY 2040 TTTCAATTCCTGCTTCCATCCAGTGTTTTACAGCTTTTCTGCTTCAATGTGAATTCACAT 2099
Db 2467 TTTCAATTCCTGCTTCCATCCAGTGTTTTACAGCTTTTCTGCTTCAATGTGAATTCACAT 2526
QY 2100 ACACTCTCATTTTCTCTCATCAACAACCCCAAGTGACCAATGCTCTCATTTGATATA 2159
Db 2527 ACACTCTCATTTTCTCTCATCAACAACCCCAAGTGACCAATGCTCTCATTTGATATA 2586
QY 2160 AGTAAAGAGAGCTCTGCAATTAAAGGCTGTGCCAAGGACGCACTGAGAGGCGCTAGAC 2219
Db 2587 AGTAAAGAGAGCTCTGCAATTAAAGGCTGTGCCAAGGACGCACTGAGAGGCGCTAGAC 2646
QY 2220 TGGCTCCATTTCCATCTGTATTTCTCACTGACTTTGACTACCAAGCCCAACATGTGGG 2279
Db 2647 TGGCTCCATTTCCATCTGTATTTCTCACTGACTTTGACTACCAAGCCCAACATGTGGG 2706
QY 2280 GCGCTCAGTATTCGATCAATTAATTTCTAATTAAGAGCAAAAACAATTCGCCGATGGCCCC 2339
Db 2707 GCGCTCAGTATTCGATCAATTAATTTCTAATTAAGAGCAAAAACAATTCGCCGATGGCCCC 2766
QY 2340 AGTTATTAAGCATTTCTCAGATTTTACCTTGAGAAATGCCATCGGCTGTATATTCACAT 2399
Db 2767 AGTTATTAAGCATTTCTCAGATTTTACCTTGAGAAATGCCATCGGCTGTATATTCACAT 2826
QY 2400 CTTCACCTGTGTCCCTTCTCTCAGAAAAGGAGAAAGTCAAGTGAATGCCCTTGAGAAC 2459
Db 2827 CTTCACCTGTGTCCCTTCTCTCAGAAAAGGAGAAAGTCAAGTGAATGCCCTTGAGAAC 2886
QY 2460 TAGTGCATGGCTTAACGTGCTTCCATGACTCCGTGCTATCTGTTTCTAATTTCTCC 2519
Db 2887 TAGTGCATGGCTTAACGTGCTTCCATGACTCCGTGCTATCTGTTTCTAATTTCTCC 2946
QY 2520 TTTTCCACCGAAGTCTATAATCTCAAGAAAAGCAGGCACTGGCCTTAGGGCTCCTGGCT 2579
Db 2947 TTTTCCACCGAAGTCTATAATCTCAAGAAAAGCAGGCACTGGCCTTAGGGCTCCTGGCT 3006
QY 2580 AAGAAATATCAAGTCCAGTGAGAAATCCCAATGACTGACCCCTCTGCTTACCCCTTGT 2639
Db 3007 AAGAAATATCAAGTCCAGTGAGAAATCCCAATGACTGACCCCTCTGCTTACCCCTTGT 3066
QY 2640 GATGGAAGACTCCAGGGGTTGCTTTTTCATGTTACAGGCTTAACCTCAGCATCAC 2699
Db 3067 GATGGAAGACTCCAGGGGTTGCTTTTTCATGTTACAGGCTTAACCTCAGCATCAC 3126
QY 2700 AGGGGCAAGAAAAGGAAAGTAACTTAATGCTGCTTAATTTGAATTTGAAT 2759
Db 3127 AGGGGCAAGAAAAGGAAAGTAACTTAATGCTGCTTAATTTGAATTTGAAT 3186
QY 2760 AGTTAATTACTGTGATTTGTACATGTGTAAACAGCAAAATGTGTATTTTTCACAGCTGC 2819
Db 3187 AGTTAATTACTGTGATTTGTACATGTGTAAACAGCAAAATGTGTATTTTTCACAGCTGC 3246
QY 2820 TGTGATTTGATTATGCTCAATTTGGAATTAAGATGCTGTTAAGACACACAAGCCAGGTTT 2879
Db 3247 TGTGATTTGATTATGCTCAATTTGGAATTAAGATGCTGTTAAGACACACAAGCCAGGTTT 3306
QY 2880 CTCAAGTCGTAGCAAAATTTTCAAAAAGTTAAATTTAAATTTAAATTTCACTTGAATCTAG 2939
Db 3307 CTCAAGTCGTAGCAAAATTTTCAAAAAGTTAAATTTAAATTTCACTTGAATCTAG 3366
QY 2940 TGACAGAGAAATGACATGATAGAGACTAAAGATCTAGCCCAATTTTATATTACTT 2999
Db 3367 TGACAGAGAAATGACATGATAGAGACTAAAGATCTAGCCCAATTTTATATTACTT 3426
QY 3000 GTTAGAGATTTTGAACAATTTACTAAATTTCTCAAGGTTCAATTTCCCATTAATCTAT 3059
Db 3427 GTTAGAGATTTTGAACAATTTACTAAATTTCTCAAGGTTCAATTTCCCATTAATCTAT 3486

QY 3060 AATGAATGTCATCATTAATGGGCCCCGAGAGACATAATTACTGTAAATGTAATAAT 3119
Db 3487 AATGAATGGCTCATCATTAATGGGCCCCGAGAGACATAATTACTGTAAATGTAATAAT 3546
QY 3120 CATGTGTTATTAATTAATACATATTTGCTTTAAATGATAAGATTTTAAAGGTATAT 3179
Db 3547 CATGTGTTATTAATTAATACATATTTGCTTTAAATGATAAGATTTTAAAGGTATAT 3606
QY 3180 GTAAACTGTAAACATAAATGCAAAATGCCGTAAGACACATATAATATAATGATTA 3239
Db 3607 GTAAACTGTAAACATAAATGCAAAATGCCGTAAGACACATATAATATAATGATTA 3666
QY 3240 TTATATTTGTTATCATTAATCTAGCTGTTTTTCTGTTGTAATTTCTTCTTAAATGC 3299
Db 3667 TTATATTTGTTATCATTAATCTAGCTGTTTTTCTGTTGTAATTTCTTCTTAAATGC 3726
QY 3300 TTACAGAAATCTGTATCCCAATCTTCAACCAACCCCAACAATTTCTGCTTCTTCC 3359
Db 3727 TTACAGAAATCTGTATCCCAATCTTCAACCAACCCCAACAATTTCTGCTTCTTCC 3786
QY 3360 CATGCC-GGTCAATGTAATCTTGAAGCTTCAGCTCTTCTCTCAATCTCTCTG 3418
Db 3787 CATGCCGGGCTCATGCTAATCTTGAAGCTTCAGCTCTTCTCTCAATCTCTCTG 3846
QY 3419 GCACTCTGATATGCTTTGAATTCATGTTAAAGAAATCCCTAGGCTGCTATCAATGT 3478
Db 3847 GCACTCTGATATGCTTTGAATTCATGTTAAAGAAATCCCTAGGCTGCTATCAATGT 3906
QY 3479 GGCATCTTGTGTAGTACATGAATAATCACTGTTGTTTTCGAAGATGATATGC 3538
Db 3907 GGCATCTTGTGTAGTACATGAATAATCACTGTTGTTTTCGAAGATGATATGC 3966
QY 3539 TTCATTTGGGATGTTATTTTCTTCTCTATCACAGGAGAAAGTGAA 3586
Db 3967 TTCATTTGGGATGTTATTTTCTTCTCTATCACAGGAGAAAGTGAA 4014

RESULT 5

US-10-311-455-310/c
; Sequence 310, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determining the Cytosine Methylation
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311,455
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 310
; LENGTH: 7201
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-310

Query Match 67.1%; Score 2406; DB 6; Length 7201;
Best Local Similarity 80.6%; Pred. No. 0;
Matches 2889; Conservative 0; Mismatches 685; Indels 12; Gaps 6;

QY 3 ATCCCTACCTTCCCATCAGAGCTGAGGGGCGATGAGCGCTCTGCTAAGATGGGACC 62
Db 5746 ATCCCTACCTTCCCATCAAAACATATAAAACGCTCTACTATAAATAAACC 5687

QY 63 CCAGAGAAATGTCCTCCCTGTTGGGCACTTCTTACCAATGGATGGCCAGTGGGTTAA 122
Db 5686 CCAGAGAAATGTCCTCCCTAT-AAACACTTCTTACCAATGAATAAACAATACAAATTA 5628
QY 123 GTTGTGTGTGAGGAG 182
Db 5627 ATTAATAATCAACAG 5668
QY 183 TCAATGAGATGGGAG 242
Db 5567 TCAATGAGATGGGAG 5508
QY 243 AAAAGTGCATAGCTGGGCGAGGCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 302
Db 5507 AAAAATACATTAACCTTAAC--GCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5451
QY 303 GGGCTCTCATTTCCAGCCCAAG 362
Db 5450 AACTCTCCATTTCCAGCCCAAG 5391
QY 363 CAACCAACCAAG 422
Db 5390 CAACCAACCAAG 5331
QY 423 AGCAGACACCAATCATTAATAATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 482
Db 5330 AACCAACCAATCATTAATAATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5271
QY 483 CTGCCCCATGTCTCAAGTTGAGTGGGCCCCCTCTCTCCAGATCTCTGCCACCATCTTAGAA 542
Db 5270 CTGCCCCATGTCTCAAGTTGAGTGGGCCCCCTCTCTCCAGATCTCTGCCACCATCTTAGAA 5211
QY 543 GGAACACTGAAG 602
Db 5210 AAGCACTGAAG 5151
QY 603 CTAAATCATTTGTTCAATGAATGAATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 662
Db 5150 CTAAATCATTTGTTCAATGAATGAATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5091
QY 663 TGTGAATCTTTTCTGCTATCCAG 722
Db 5090 TGTGAATCTTTTCTGCTATCCAG 5031
QY 723 TTGAGAGCTAAAGATCATTTGAGATTTCACTGCTGAGTTGATTTGATTTGATTTGAT 782
Db 5030 TTGAGAGCTAAAGATCATTTGAGATTTCACTGCTGAGTTGATTTGATTTGATTTGATTTGAT 4971
QY 783 TGAACCTCAC-TTGTAAATCTGACACGAGGCAATCAATCTGACAGAGAGATATGT 841
Db 4970 TGAACCTCAC-TTGTAAATCTGACACGAGGCAATCAATCTGACAGAGAGATATGT 4916
QY 842 TAAACAGTGTAAATGCTGATGAG 901
Db 4915 TAAACAGTGTAAATGCTGATGAG 4856
QY 902 TTTCTTTCTTATTTGTTCTTACTTATTTTACGATTACCCGATGCTTTTCCCAAAATGTAAGAG 961
Db 4855 TTTCTTTCTTATTTGTTCTTACTTATTTTACGATTACCCGATGCTTTT-CCAAATATTAAGAG 4797
QY 962 GCCATTTGAAAGCCTAATCAAACTCTTCACTAATTTGATCTAAGTATTCACCTTGA 1021
Db 4796 ACCATTTTAAAGCCTAATCAAACTCTTCACTAATTTGATCTAAGTATTCACCTTGA 4737
QY 1022 TTGAGAGCTGGTGAAG 1081
Db 4736 TTGAGAGCTGGTGAAG 4677
QY 1082 TTTATTTATTTATTTATTTTGAAGATGAGTCTGGCTGCTGCCAGGCTGAGTGCAGC 1141
Db 4676 TTTATTTATTTATTTATTTTGAAGATGAGTCTGGCTGCTGCCAGGCTGAGTGCAGC 4617

QY	1142	GGCGTGATCACAGTTCACTGCAGCCTCAACCTTCTAGGCTCAAGGAGTTCTCCACCTCA	1201
Db	4616	GACGTAATCACAAATTCATACAACCTCAACCTTCTAATCTCAAAAAATTCCTCACCTCA	4557
QY	1202	GCCCCCAAGTAGTTGGGACCAACGATGCGCCACCATGCGTGGTAAATTCCTAATTTT	1261
Db	4556	ACCCCCCAAAATATTAACAACAACGATATACGCCACCACTAACCTAATTCCTAATTTT	4497
QY	1262	TTTGTAAGATAGATCTCACTATATTGTCCAGGCTGTGCTTGAATTCCTGGGCTCAGT	1321
Db	4496	TTTATAAAAATAAAATCTCACTATATTATCCAAACTAATCTTAAATTCCTAAACTCAAT	4437
QY	1322	GAGCCTCCACCTGGGCTCCCAAAGTACTGGATTAAGGATGAGCCAAAGTCCCTG	1381
Db	4436	AAACCTCCCACTAAACCTCCCAAATACTAAAATTACAAACATAAACCAAAATCCCTA	4377
QY	1382	CCCATATGAGATTTTCTGTCTCTGATCCCATGCACTAGTAATCAAGACTTGGCTGTG	1441
Db	4376	CCCATATAAAAATTTCTATCTCTAATCCCATACACTATATATCAAAAACTTAACCTA	4317
QY	1442	ACTCTGAGAGACCTGCATGCTTCTTGAGCTGTGAACCTTCACTGCTAAAGCTCATAGGC	1501
Db	4316	ACTCTAAAAAACCTACATACCTTCTTAAACTATTAACCTTCAATACCTAAAACTCA	4257
QY	1502	AGCCTGAAAACCCAAACCAAAAGSTCTATGTTTATCATCTGATCATGTTGATTTTAT	1561
Db	4256	AACCTAAAAACCCAAACCAAAAAATCTATATTTTATCATCCGATCATATTTAATTTAT	4197
QY	1562	AGAAATAACACATGAATTAAAGACATACCTCAAACTGACCAAACTTAAGTAATTTT	1621
Db	4196	AAAAATAACACATTAATTAATAACACTACCTCAACCTAACAACAACTTAATTAATTTT	4137
QY	1622	TTAAAGTTGACCTGTTTAAATCACTCTTGGAGAAAAAGAAAATAAATACAAATAAT	1681
Db	4136	TTAAATTTAACCTATTTTAAATCACTCTTAAAAAAAATAAATAAATAAATAAT	4077
QY	1682	TAAAGGTGAATACAGGCTATACCTTGTCTCCAGAAATTAGCACTTGTCTTTTC	1741
Db	4076	TAAAGATAAATACAAACTACTATACCTTATTTCCAAAATTAAACAATTCTATCTTTTC	4017
QY	1742	TGCTTTAGATGCTGAAGTGCAGAAAGACACTCTGTCATGTTGTACGTTGTAACGCAAA	1801
Db	4016	TTACTTTAAATACTAAATAACAAAAAACACTCTATTAATTATACGTATATTAACAA	3957
QY	1802	ATGTGATTTTTTTCTCAGCTGCTATGATTTGATTAATGCTATTATGAATAAAGATGCT	1861
Db	3956	ATATATATTTTTTTCTCACTACTATAAATTAATTAATTAATTAATAAATAAATACT	3897
QY	1862	GATGGAGCACACACAACCAATTTGTTCTCAGTCCATTTTCTCCTCAAAAGCTGGAA	1921
Db	3896	AATAAAAACACACACAACAACCAATTTATCTCTCAATCCATTTCTCCTCAAAAACCTAAA	3837
QY	1922	TGTGCCATTGATCAGTGGAGATGTACCTGACAGACCCATGAATAAGAGATCAACAAT	1981
Db	3836	TATACCAATTAATCAATAAAAAATATACCTAAACAACCCATTAATAAAAAAATCAACAAT	3777
QY	1982	CCACCCCAAGGAGCCCTATTTTCTTAATTTCAATTTGAATGGCTCTAATTTGCTCTT	2041
Db	3776	CCACCCCAAAAAACCCCTATTTTCTTAATTTCAATTTAATAATTAACCTTAATTTCTT	3717
QY	2042	TCAATTCCTGCTTCTCCTACCAAGTTTACAGCTTTTCTGTTCAAATGTGAACCTACATAC	2101
Db	3716	TCAATTCCTACTTCTCCTACCAATTTTACAACTTTTCTTAATTTCAAAATATAAAGCTACATAC	3657
QY	2102	ACTCTCATTTTTCTCTCATCAACAACCCCAAGTGACCCCAATGTCCTCACTTTCGATATAAG	2161
Db	3656	ACTCTCATTTTTCTCTCATCAACAACCCCAATTAACCCCAATATATCCTCACTTTCGATATAAA	3597
QY	2162	TAAAGGAGGCTCTGCATTAAGGCTGTGCCAAGGCAACGACGTGAGAAGGCGTAAAGACTG	2221
Db	3596	TAAAAAAAACTCTACATTTAAAAAATTAATCCAAAAACGCACTAAAAAAACGCTAAAACTA	3537
QY	2222	GCTCCATTTCCATCTCTATTTCTCACTGACTTTGACTTACCCAGAAACCCCAACATGTGGGC	2281

Db	3536	ACTCCATTTCCATCTCTATTTCTCACTAACTTTAACTAACCCAAAACCCCAACATATATAAAAC	3477
Qy	2282	CTCAGTATTCGATCAATTAATCTATTAAGAAGCAAAAACAATTCGCCGCAATGGCCCCAG	2341
Db	3476	CTCAATATTCGATCAATTAATCTATTAATAAAACAACAAATTCGCCGCAATTAACCCCAA	3417
Qy	2342	TTATTTAAGCATTTCTCAGATTTTACCTTGAGAAATGCCATCGGCGTGTAATTTCACATCT	2401
Db	3416	TTATTTAACAATTTCTCAAAATTTTACCTTAATAAAATACCCATCGACCTATATATTCACATCT	3357
Qy	2402	TCACCCCTTGTCCTTCTCTCTAGAAAAGGAGAAAGTCAAGTTGGATGCCCTCTGAGAACTA	2461
Db	3356	TCACCCCTTATCCCTTCTCTCTTAAAAAAAATAAAAAATCAATTTAAATACCCCTTAATAAACTA	3297
Qy	2462	GTGCATGGCTTAACCTGTCTCTCCATGACTCCTGCGCTTATCTGTTTCTATTTCTCTCTT	2521
Db	3296	ATACATTAACCTTAACCTTCTCTCCATTAACCTCTTACCTTATCTATTTCTCTCTCT	3237
Qy	2522	TTCCACCGAAGTCTAATTAATCTCAAGAAAAAGCAGGCACTGGCCTTAGGGCTCTGGCCTAA	2581
Db	3236	TTCCACCGAAGTCTAATTAATCTCAAAAAAACAACACTAACCTTAACCTTAACCTTAA	3177
Qy	2582	GAAATATCAAGTCCAGTGAAGAAATCCCATTTGACTGACCCCTCTGCTTACCCCTTTGTGA	2641
Db	3176	AAAATATCAAAATCCAAATAAAATCCCATTTAATAACCCCTCTACTACCCCTTATAA	3117
Qy	2642	TGGAGAAGCTCCCAAGGGGTTGCTTTTGCATGTTTACCAGGCTTAACCTCAGCATCACCAAG	2701
Db	3116	TAAAAAACTCCCAAAATTTACTTTTACATATTTACCAAACTTAACCTCAACATCACCAA	3057
Qy	2702	GGGCAAGAAAAGGAAAGTAACTTAACCTTAATGCTGCTTATTAATTTGTAATTTGTAATAG	2761
Db	3056	AAACAAAAAATAAAATAAACTTAACCTTAATTAATTAATTAATTAATTAATTAATTAATTA	2997
Qy	2762	TTAATTACTGTGATTTGTACATGTGTAAACAGACAAATGTGTATTTTTCACAGCTGCTG	2821
Db	2996	TTAATTACTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTTTTCACACTACTA	2937
Qy	2822	TGGATTGATTATGCCATTTTGAATTAAGAATGCTGTAAAGACACACAAGCCAGTTCCT	2881
Db	2936	TAAATTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	2877
Qy	2882	CAAGTCCGTAGCAAAATTTTCAAAAAGTTAAATTTAAATTAATTAATTAATTAATTAATTAAT	2941
Db	2876	CAATCCGTAAACAATTTTCAAAAATTTAAATTTAAATTAATTAATTAATTAATTAATTAAT	2817
Qy	2942	ACAGGAGAAATGACATGGATAGAGACTAAAGATCTAGCCCAATTTTATATTTACTTGT	3001
Db	2816	ACAAAAAATAAACTAAATTAATAAACTTAATAAACTTAATAAACTTAATAAACTTAATAAT	2757
Qy	3002	TAGAGGATTTTGAACAAATTAATAATTTCTCAAGGTTCAATTTCCCCATTAATACTATAA	3061
Db	2756	TAAAAAATTTTAAACAATTAATAATTTCTCAAAATTTCAATTTCCCCATTAATACTATAA	2697
Qy	3062	TGAATGTCTCATTAATGGGGCCCTGAGAGAGCAATAATTAATTAATTAATTAATTAATTAAT	3121
Db	2696	TAAATACTCATTAATAAAACCCCTAAAAAAACATAATTAATTAATTAATTAATTAATTAAT	2637
Qy	3122	TTGTTATTTATTAATTAATTAATTTTGTCTTTAAATGGAATAAGGATTTTAAAGTATATGT	3181
Db	2636	TTATTTATTTATTAATTAATTAATTTTACTTTTAAATTAATAAAATTTTAAATTAATTAAT	2577
Qy	3182	AAACTGTAAAAACATAAATGCAAAATGCCGTAAAGACAGTAGTAATTAATTAATTAATTT	3241
Db	2576	AAACTATAAAAACATAAATTAACAAATACCGTAATAAAACAAATTAATTAATTAATTAATTT	2517
Qy	3242	ATATTTGTATCATTAATTAAGCTGTTTTCCTGTTGTATTTCTTCTTTAAATGCTT	3301
Db	2516	ATATTTATTTATCATTAATTAAGCTGTTTTCCTGTTGTATTTCTTCTTTAAATGCTT	2457
Qy	3302	ACAGAAATCTGATCCCATCTTTCACCAACCAACCAACCAATTTCTGCTTTTCCCA	3361

Db 2456 TCAAAATCTATATCCCATCTTTCACCAACCACCAACATTTCTACTTCTTTCCCA 2397
Qy 3362 TGCCG-GTCATGCTAACTTTGAAAGCTTCAGCTCTTTCCTCTCAATCCTTCCTGGC 3420
Db 2396 TACCGAATCACTACTAACTTMAAACTTCAACTCTTCCCTTCAATCCTTTCCTAAC 2337
Qy 3421 ACCCTGATATGCCCTTTGAAATTCATGTTAAAGATCCCTAGGCTGCTATCACATGG 3480
Db 2336 ACCCTAATATACCTTTTAAATCATATTAATAATCCCTAACTACTATCACATATA 2277
Qy 3481 CATCTTGTGAGTACATGAATAATCAACTGCTGTGTTTACGAAGATGATATGCTT 3540
Db 2276 CATCTTATTAATACATAATAATAATCAACTAATATATTTACGAAAAATATATACTT 2217
Qy 3541 CATGTGGGATGTATTTTCTTCTTCTATCACAGGAGAGTGA 3586
Db 2216 CATTAATAAATATATATTTTCTTCTTCTATCACAAAAAAATATA 2171

RESULT 6
US-10-311-455-309
; Sequence 309, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
; TITLE OF INVENTION: cytosine methylation
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311,455
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 309
; LENGTH: 7201
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-309

Query Match 63.4%; Score 2271.8; DB 6; Length 7201;
Best Local Similarity 78.2%; Pred. No. 0;
Matches 2805; Conservative 0; Mismatches 772; Indels 10; Gaps 6;
Qy 1 GGATCCCTACCTTCCCATCAGAGCTAGGGGGCATGAGCGCTCTGCTAAGATGGGA 60
Db 1454 GGAATTTTATTTTATTTAGAGTTAGGGGGTATGAGCGCTTTTGTAAAGATGGGA 1513
Qy 61 CCCCCAAGGAATGTCTCCCTGTGGGCACTTCTTACCAGATGGGATGGCAGTGGTT 120
Db 1514 TTTTAAAGGAATGTTTTTGT-GGGTAATTTTATTTAGATGGATGGTATGTAATT 1572
Qy 121 AAGTGTGTGTCAGGCAGAAAAAAGATCTAGTTGTACTCTTGAGAGTTCCGCTT 180
Db 1573 AAGTGTGTGTCAGGCAGAAAAAAGATCTAGTTGTACTCTTGAGAGTTTTCGCTT 1632
Qy 181 GTTCATGCGATGGGAGGAGTCAAGACAGCAGCGCTTGCTCAGTGCCTACAGTGA 240
Db 1633 GTTATGATATGGGTAGGAGGAGTAAAGAGTAGTAGTTTGTAGTTAGTTATAGTGA 1692
Qy 241 GGAAGAGTGCATAGCCTGGGCGAGGGCCAGGGCCCTGTGTGAGCGGTAGTGTAACA 300
Db 1693 GGAAGAGTGCATAGCCTGGGCGAGGGCCAGGGCCCTGTGTGAGCGGTAGTGTAACA 1749
Qy 301 GAGGCTCTCATTCAGCCCAAGAGAGCTAAGATGAATCTCATGATATATAGC 360

Db 1750 GAGGTTTTTATTTAGTTAAGAGAGATTAGAATGAATTTATGAGTATATAGT 1809
Qy 361 TACAAACCAACAGACAGAGTTCCAGAAAAAGGCTCAGCGTTGGAACAGTCACCCCAC 420
Db 1810 TATTAATTAATTAATAGTAGGTTTGAAGAAAAAGGTTAGCGTTGGAATTAAGTTAT 1869
Qy 421 TCAGAGACACCAAGTCAATATAATCAAGGACCAACAGAGACAGGAACACCCCTTCCCA 480
Db 1870 TTAGTATATTAATAGTATATAATTAAGGATTAATAGAGATAGGAATATTTTTTTTA 1929
Qy 481 CTCTGCCCATGTCTCAAGTTGAGTGGCCCTTCTCCAGATCTCTGCCACCATCTTGA 540
Db 1930 TTTTGTTTATGTTTAAAGTTAGTGGTTTTTTTTTTAGATTTTGTATATTTTGA 1989
Qy 541 AAGAACACTGAAGAAGAACTGAATTTAAGCTGACAGCATAAAGAGATGATAA 600
Db 1990 AAGGAATATTGAAGAAGAAATGAATTTAAGTTGATGATATAAGAGATGAGTAA 2049
Qy 601 ACCTAAATCATTTGTCATGATGATCAAGATCAAGAGAGTTTAAACCACTTGACTAAA 660
Db 2050 AATTAAATTAATGTTTAAATGAATGAATTAAGAGAGAGTTTAAATTAATTTGATTA 2109
Qy 661 TGCTGAATCCTTTTCTGCTATCCAGCAGATGAGAACTGTGTAACAGACACACATA 720
Db 2110 TGCTGAATTTTCTTTTCTGCTATTTAGATGAGAACTGTGTAATAGATTAATA 2169
Qy 721 GTTGGAGACTAAGAAATGATGACATTTCACTGCTGAGTTGATGTGATTAATTGA 780
Db 2170 GTTGGAGACTAAGAAATGATGATTTATTTATTTATTTATTTATTTATTTATTTA 2229
Qy 781 GTTGAACCTCACTTGTAAATCTGCAACAGGGGCAATCCAATATCTGACACAGAGATAG 840
Db 2230 GTTGAATTTATTTTGTAAATTTTGTATACGGGTATTTAATTTGT--ATAGAGATAG 2286
Qy 841 TTAACAGTGTAAATGCTGATGAGAGAGATTTGGGTGATTTTACTTCTTTTGTGCT 900
Db 2287 TTAATAGTGTAAATGCTGATGAGAGAGATTTGGGTGATTTTACTTCTTTTGTGCT 2345
Qy 901 CTCTTCTTATTTGTTCTTACTTATTTACGATTACCTTACCTTCTTCCAAATGTAAA 960
Db 2346 TTTTATTTTATTTGTTTATTTATTTATTTACGATTATTTATTTATTTATTTATTT 2404
Qy 961 GGCAATTTGAAGCCCTAATCAACCTCTTCACTATTTGTATCTAAGTATTCACCTTG 1020
Db 2405 GGTATTTTGAAGTTAATTTAATTTTATTTATTTATTTATTTATTTATTTATTTAT 2464
Qy 1021 ATTGAAGTGGGTAGACAGGTGAAACCAATATCAGGTTTAAATTTTAAATTTTAA 1080
Db 2465 ATTGAAGTGGGTAGACAGGTGAAACCAATATATTTAGGTTTAAATTTTAAATTT 2524
Qy 1081 ATTATTTATTTATTTATTTTGAAGATGAGTCTGCTGCTGCTGCTGCTGCTGCTG 1140
Db 2525 AATTATTTATTTATTTTGAAGATGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTG 2584
Qy 1141 CGGCGTATCACAGTTCACTGACCTCAACCTTCTAGGCTCAAGGATTTCTCCACCTC 1200
Db 2585 CGGCGTATTAAGTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 2644
Qy 1201 AGCCCCCAAGTAGTTGGACACACGATGCGCCACCAAGCTTGCTAATTTCTATTT 1260
Db 2645 AGTTTATTAAGTAGTTGGACATTAACGATGCGTATTAAGTTTGGTTAATTTTATTT 2704
Qy 1261 TTTTGTAGAGATGAGATCTCATATTTGTCCAGGCTGTGTAATTTCTGGGCTCAGG 1320
Db 2705 TTTTGTAGAGATGAGATTTATTAATTTGTAGGTTGTTTGAATTTTGGGTTTAA 2764
Qy 1321 TGAAGCTCCCACTGGGCTTCCAAAGTACTGGGATTAACAGCATGAGCCAAAGTCCCT 1380
Db 2765 TGAAGTTTATTTTGGGTTTAAAGTATTTGGGATTAAGGATTAAGGTTTATTT 2824
Qy 1381 GCCCATATGAGATTTCTGCTCTGATCCCATGAGCTAAGTAAATCAAGGACTTGGCTG 1440
Db 2825 GTTATATGAGATTTTGTGTTTGAATTTATGATGATTAAGGATTTGTTGTT 2884


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RESULT 7
US-10-106-623-3
; Sequence 3, Application US/10106623
; Publication No. US20020150888A1
; GENERAL INFORMATION:
;   APPLICANT: Gray, Patrick W.
;   Schwickart, Vicki L.
;   Raport, Carol J.
; TITLE OF INVENTION: Chemokine Receptor Materials and Methods
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESSES:
;   ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
;   STREET: 6300 Sears Tower, 233 S. Wacker Drive
;   CITY: Chicago
;   STATE: Illinois
;   COUNTRY: USA
;   ZIP: 60606
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/10/106,623
;   FILING DATE: 26-Mar-2002
;   CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/771,276
;   FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
;   NAME: No. US20020150888A1and, Greta B.
;   REGISTRATION NUMBER: 35,302
;   REFERENCE/DOCKET NUMBER: 27866/33670
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 312-474-6300
;   TELEFAX: 312-474-0448
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 1915 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 362..1426
; FEATURE:
;   NAME/KEY: misc feature
;   OTHER INFORMATION: /= "88-2B polynucleotide and amino acid
;   sequences"
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
;
US-10-106-623-3
Query Match          9.6%; Score 344.2; DB 5; Length 1915;
Best Local Similarity 98.9%; Pred. No. 4.6e-67;
Matches 357; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 3227 ATAAATAATGATTATATATGTTATCATATCTAGCCGTGTTTCTGTTGTGATTTTC 3286
DB 1 ATAAATAATGATTATATATGTTATCATATCTAGCCGTGTTTCTGTTGTGATTTTC 60

QY 3287 TTCCTTAAATGCTTACAGAAATCTGTATCCCATTTCTTACACCAACCCACAACATTT 3346
DB 61 TTCCTTAAATGCTTACAGAAATCTGTATCCCATTTCTTACACCAACCCACAACATTT 120

QY 3347 CTGCTTCTTTCCCATGCGC-GGTCAAGCTAACTTTGAAAGCTTCAGCTCTTTCCTTC 3405
DB 121 CTGCTTCTTTCCCATGCGCGGTCAAGCTAACTTTGAAAGCTTCAGCTCTTTCCTTC 180

QY 3406 AATCCTTCTCTGGCACCTCTGATATGCTTTTGAATTCATGTTAAAGAATCCCTAGGC 3465
DB 181 AATCCTTCTCTGGCACCTCTGATATGCTTTTGAATTCATGTTAAAGAATCCCTAGGC 240
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QY 3466 TGCATACATGTGCGCATCTTGTGTGAGTACATGAATAATCACTGGTGTGTTTACGA 3525
DB 241 TGCATACATGTGCGCATCTTGTGTGAGTACATGAATAATCACTGGTGTGTTTACGA 300

QY 3526 AGGATGATTATGCTTCATTGGGGATTGTATTTTCTTCTATACACAGGAGAGTGA 3585
DB 301 AGGATGATTATGCTTCATTGGGGATTGTATTTTCTTCTATACACAGGAGAGTGA 360

QY 3586 A 3586
DB 361 A 361

RESULT 8
US-10-772-037-3
; Sequence 3, Application US/10772037
; Publication No. US20040230037A1
; GENERAL INFORMATION:
;   APPLICANT: Gray, Patrick W.
;   Schwickart, Vicki L.
;   Raport, Carol J.
; TITLE OF INVENTION: Chemokine Receptor Materials and Methods
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESSES:
;   ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
;   STREET: 6300 Sears Tower, 233 S. Wacker Drive
;   CITY: Chicago
;   STATE: Illinois
;   COUNTRY: USA
;   ZIP: 60606
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/10/772,037
;   FILING DATE: 04-Feb-2004
;   CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/08/771,276
;   FILING DATE: 20-DEC-1996
; ATTORNEY/AGENT INFORMATION:
;   NAME: Noland, Greta B.
;   REGISTRATION NUMBER: 35,302
;   REFERENCE/DOCKET NUMBER: 27866/33670
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 312-474-6300
;   TELEFAX: 312-474-0448
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 1915 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 362..1426
; FEATURE:
;   NAME/KEY: misc feature
;   OTHER INFORMATION: /= "88-2B polynucleotide and amino acid
;   sequences"
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
;
US-10-772-037-3
Query Match          9.6%; Score 344.2; DB 8; Length 1915;
Best Local Similarity 98.9%; Pred. No. 4.6e-67;
Matches 357; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 3227 ATAAATAATGATTATATATGTTATCATATCTAGCCGTGTTTCTGTTGTGATTTTC 3286
DB 1 ATAAATAATGATTATATATGTTATCATATCTAGCCGTGTTTCTGTTGTGATTTTC 60
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QY	3287	TTCCCTTTAAATGCTTTACAGAAATCTGTATCCCATTTCTTACCAACCACCCCAACAATTT	3346
Db	61	TTCCCTTTAAATGCTTTACAGAAATCTGTATCCCATTTCTTACCAACCACCCCAACAATTT	120
QY	3347	CTGCTTCTTTTCCCATGCC-GGTCACTAGCTAACTTTGAAAGCTTCAGCTCTTTCCTCCTC	3405
Db	121	CTGCTTCTTTTCCCATGCCGGGTCACTAGCTAACTTTGAAAGCTTCAGCTCTTTCCTCCTC	180
QY	3406	AATCCTTCTCCTGGCACCTCTGTATATGCCCTTTGAAATTCATGTTAAGAATCCTTAGGC	3465
Db	181	AATCCTTTTCCCTGGCACCTCTGTATATGCCCTTTGAAATTCATGTTAAGAATCCTTAGGC	240
QY	3466	TGCTATCACATGTGGCATCTTTGTGAGTACATGAATAAATCAACTGGTGTGTTTACGA	3525
Db	241	TGCTATCACATGTGGCATCTTTGTGAGTACATGAATAAATCAACTGGTGTGTTTACGA	300
QY	3526	AGGATGATTATGCTTCATGTGGGATTGTATTTTCTTCTATCACAGGAGAAATGA	3585
Db	301	AGGATGATTATGCTTCATGTGGGATTGTATTTTCTTCTATCACAGGAGAAATGA	360
QY	3586	A 3586	
Db	361	A 361	

RESULT 9
US-09-925-065A-727856
; Sequence 727856, Application US/09925065A
; Publication No. US20050228172A9

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? TITLE OF INVENTION: Identification and Mapping of Single
? TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
? FILE REFERENCE: 108827.135
? CURRENT APPLICATION NUMBER: US/09/925,065A
? CURRENT FILING DATE: 2001-08-08
? PRIOR APPLICATION NUMBER: US 60/243,096
? PRIOR FILING DATE: 2000-10-24
? PRIOR APPLICATION NUMBER: US 60/252,147
? PRIOR FILING DATE: 2000-11-20
? PRIOR APPLICATION NUMBER: US 60/250,092
? PRIOR FILING DATE: 2000-11-30
? PRIOR APPLICATION NUMBER: US 60/261,766
? PRIOR FILING DATE: 2001-01-16
? PRIOR APPLICATION NUMBER: US 60/289,846
? PRIOR FILING DATE: 2001-05-09
? NUMBER OF SEQ ID NOS: 957086
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 727856
? LENGTH: 3771

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ORGANISM: Homo sapiens
US-09-925-065A-727856

Query Match	6.0%;	Score 215.2;	DB 4;	Length 3771;
Best Local Similarity	72.2%;	Pred. No. 1.1e-37;		
Matches 280;	Conservative	0;	Mismatches 108;	Indels 0;
			Gaps	0;

[illegible]

Db	2141	TACAGGCACCTGGCCACCATGECCTAGCTAATTTTGTATTTTGTAGAGACAGGGGCTTCA	2200
QY	1282	CTATATTGTCCAGGCTGGTCTTGAATTCCTGGGCTCAGGTGAGCCCTCCCACTGGGCTC	1341
Db	2201	CCATGTTGGCCAGGCTGGTCTTGAATCCTGACTTCAGGTGATCCGGCCACCTTGGGCTC	2260
QY	1342	CCAAAGTACTGGGATTAACAGGCATGAGCCAAAGTCCCTGCCCCATATGAGATTTTCTGTC	1401
Db	2261	CCAAAGTACTGGGATTAACAGGCATGAGCCAAAGTCCCTGCCCCATATGAGATTTTCTGTC	2320
QY	1402	TCTGATCCCATGACGCTAGTAATCAAGG	1429
Db	2321	TTAAATCCCATCTTAAGAAAAAGCTAGG	2348

RESULT 10
US-09-925

; Sequence 804603, Application US/09925065A
; Publication No. US20050228172A9

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; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925, 065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243, 096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252, 147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250, 092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261, 766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289, 846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 804603
; LENGTH: 606
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-804603

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Query Match	5.9%;	Score 212.4;	DB 4;	Length 606;
Best Local Similarity	72.6%;	Pred. No. 1.8e-37;		
Matches 273; Conservative	1;	Mismatches 102;	Indels 0;	Gaps 0;

QY	1023	TGAGACTGGGTAGACAGGTGAAAAACCATATCAGGTTTTTAATTTTAAATTTTAAATTTAT	1082
Db	103	TGGGAAAGAGTTCTAAGCTCTAATTTCTTTTCTTTTAAATTTAATTTAATTTAT	162
QY	1083	TTATTTATTTATTTATTTTGTGAGATGAGTCTGGCTGTGCCAGGCTGAGTGCAGCG	1142
Db	163	TTATTTATTTATTTATTTGAGATGAGTCTGTCTCTGTGACCCAGGCTGAGTGCAGTG	222
QY	1143	GCGTGATCACAGTTCACATGACGCTCAACCTTCTAGGCTCAAGGATTTCTCCACCTCAG	1202
Db	223	GCATGATCTCAGCTCACATGCAACCTGTGCTCTGGGTTTAAAGACATTTCTCCTGCTCAG	282
QY	1203	CCCCCAGTAGTGTGGGACCAACGATATGCGCCACCAATGCTGCTAATTTCTTAATTTT	1262
Db	283	CCTCCCAAGTAGCTGGGATTAACGGCAACGCCACCACTGCTGGCTAATTTTGTGATTTT	342
QY	1263	TTGTAGAGATAGGATCTCACTATATTTGTCCAGGCTGTGTAATTTCTGGGCTCAGGTG	1322
Db	343	TAGTAGAGACGGGTTTAAACATGTGGCCAGGCTGTCTGAACTCCTGACCTCAGGTG	402
QY	1323	AGCCTCCACCTGGGCTGCCAAAGTACTGGGATTACAGGCATGAGCCAAAGTCCCTGC	1382
Db	403	TTCCACCCACCTCGGCTCCCAAAGTGTGGGATTACAGGCGCRAGCCAAATGCACCCGGC	462
QY	1383	CCATATGAGATTTTCT	1398

QY	1109	GGAGTCTGGCTGTTCGCCAGGCTGAGTGCAGCCGGCGTGATCACAGTTCACTGCAGCCTC	1168
Db	2852	CGTTTGTCTGTTCGCCAGGCTGAGTGCAGTGGCGGTGATCTCAGCTCACTTCACTTC	2793
QY	1169	AACCTTCTAGGCTCAAGGATTCCTCCACCTCAGCCCCCAAGTAGTTGGGACCAAGT	1228
Db	2792	CACCTTCAGGTTCAAGTGATTCCTCCTACCTCAGCCTCCGAGTAGCTGGAATTACAGAT	2733
QY	1229	ATGCGCACCAAGCGCTGGCTAATTTCTATTTTTTTGTAGATAGATCTCACTATAT	1288
Db	2732	GCATGCCACCATGCGCTGGCTAATTTATGTATTTTGTAGAGATGGGGTTTCAACAATGT	2673
QY	1289	GTCCAGGCTGTCTTGAATTCCTGGGCTCAGGTGAGCTCCACCTGGGCTCCCAAGT	1348
Db	2672	GGCCAGGCTGTCTCGAACTCCCCGGCCCCAAGTATCCGCGCCGCTCAGCCTCCCAAGT	2613
QY	1349	ACTGGGATTACAGGCAATGAGCCCAAGTCCCTGCCCCCATATGAGATTTTCTGTCTGTATC	1408
Db	2612	GTTGGGATTACAGGCAATGAGCCCACTGTGCTGGCCTTCTAGACTGTTACTTAATTGGGTC	2553
QY	1409	CCATGCAGCTAGTAATCAAGGACTTGGCTGCTGACTCTG	1447
Db	2552	TTTTGAACATATATTTTAGGCACTTCTTTATTAACCTTG	2514

RESULT 14
US-10-087

; Sequence 946, Application US/100871922
 ; Publication No. US20020182586A1
 ; GENERAL INFORMATION:

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; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for windows Version 4.0
; SEQ ID NO 946

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; LENGTH: 54701
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1) ..(54701)
; OTHER INFORMATION: n = A,T,C or G
US-10-087-192-946

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Query Match	5.9%;	Score 211.8;	DB 5;	Length 54701;
Best Local Similarity	70.7%;	Pred. No. 2.7e-36;		
Matches 282;	Conservative	0;	Mismatches 117;	Indels 0;
				Gaps 0;

[illegible]

QY 1289 GTCCAGGCTGGTCTTGAAATTCCTGGGCTCAGGTGAGCCTCCCACTGGGGCTCCCAAAGT 1348
| | | | | | | | | | | | | | | | | | | | | |
Db 38138 GGCACAGCTGGTCTCGAACTCCCGGCCCAAAGTATCCGGCGCTCAGCCTCCCAAAGT 38197

QY 1349 ACTGGATTACAGGCATGAGCCAAAGTCCCCCTGCCAATAGAGATTTCTGTCTTGATC 1408
| | | | | | | | | | | | | | | | | | | | | |
Db 38198 GTTGGATTACAGGCATGAGCCAACTGTGCTGGCCTTCTAAGCTGTACTTAATGGGTC 38257

QY 1409 CCATGCAGCTAGTAATCAAGGACTTGGCTGCTGACTCTG 1447
| | | | | | | | | | | | | | | | | | | | | |
Db 38258 TTTTGAACATAATTTTAGGCAACTTCTTTATAACCCTG 38296

RESULT 15
US-10-719

; Sequence 6833, Application US/10719993
 ; Publication No. US20040265849A1
 ; GENERAL INFORMATION:

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; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6833
; LENGTH: 60316
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-6833

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ORGANISM: Homo sapiens
US-10-719-993-6833

Query Match	5.9%;	Score 211.8;	DB 8;	Length 60316;
Best Local Similarity	70.7%;	Pred. No. 2.8e-36;		
Matches 282;	Conservative 0;	Mismatches 117;	Indels 0;	Gaps 0;

OY	1049	ATATCAGGTTTAAATT	TTTTTAATT	TAAATT	TATTAT	TATTAT	TATTAT	TATTAT	TTTGGACAT	1108
Db	46727	ATTGTGTGTTTATCTA	CTAAATG	TATTAT	TATTAT	TATTAT	TATTAT	TATTAT	TGAGACATCAAT	46786
OY	1109	GGAGTCGGCTGTCCGC	CAGGCTGA	GCTGCA	GCGGCTGATCA	CAGTTCA	CTGACGCTC			1168
Db	46787	CGTTTGCTCTGTCCGC	CAGGCTGA	AGTCA	GTGCGCTGATCT	CAGCTCA	CTCACCTC			46846
OY	1169	AACCTTCTAGGCTCAA	GGGATTCT	CCA	CTCAGCCCCCA	AGTAGTTGGGACC	CACAGT			1228
Db	46847	CACCTTCAAGTTCAAG	TGATTCT	CTAAC	CTCAGCCTCCGAGTAG	CTGGAATTACAGAT				46906
OY	1229	ATGCCACCAATGCTGT	GCTAATTTCT	TATTTTTTT	TGTAGA	TAGATGATCTCA	CTATAAT			1288
Db	46907	GCATGCCACCATGCTG	CTGCTAATTAT	TATGTA	TTTTTAGTAGATGGG	TTTCA	CCATGTT			46966
OY	1289	GTCAGGCTGGTCTTGA	ATTTCC	TGGGCTCA	BGTGAGCCTCCCA	CTGGGCTCCCA	AGT			1348
Db	46967	GGCCAGGCTGGTCTGA	ACTCCCGGCCCA	AGTAGATCCGCGCTC	CAGCCTCCCA	AGT				47026
OY	1349	ACTGGATTACAGGCAT	GAGCCAA	GGTCCC	TGCCATATGAGATTTT	CTGTCTGATC				1408
Db	47027	GTTGGATTACAGGCAT	GAGCCAT	GTGCTG	GGCTTCTAGACTGT	TACTTAAT	TGGGTC			47086
OY	1409	CCATGCAGCTAGTAAT	CAAGGACT	TGGCTG	CTGACTCTG					
Db	47087	TTTTGAACATATATTT	TAGGCAACTT	CTTTAT	TAACCTG					47125

Search completed: January 7, 2006, 20:31:28
Job time : 2608.82 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using bw model

Run on: January 7, 2006, 05:45:42 ; Search time 13084.4 Seconds
(without alignments)
12822.754 Million cell updates/sec

Title: US-10-767-521-3

Perfect score: 3586

Sequence: 1 ggatccctaccttcccccac.....ctatcacaggagaagtga 3586

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST: *
1: gb_est1: *
2: gb_est2: *
3: gb_est3: *
4: gb_hic: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_est7: *
9: gb_gss1: *
10: gb_gss2: *
11: gb_gss3: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	267.6	7.5	549	9 AQ838273	AQ838273 HS_4712_A
C 2	210	5.9	453	2 BB677425	BB677425 7d84b05.x
C 3	210	5.9	700	10 AG114100	AG114100 Pan trogl
C 4	209.6	5.8	450	9 AQ035000	AQ035000 CIT-HSP-2
C 5	208	5.8	945	5 BU527620	BU527620 AGENCOURT
C 6	207.4	5.8	6345	4 HSM805983	BX537877 Homo sapi
C 7	206.8	5.8	718	9 AQ898001	AQ898001 HS_3135_A
C 8	205.8	5.7	697	9 BZ606546	BZ606546 WHABF19TR
C 9	205.6	5.7	686	9 BZ772437	BZ772437 mcv36f03.
C 10	205.2	5.7	501	5 BX485916	BX485916 DKFZp686E
C 11	204.8	5.7	533	7 CN274852	CN274852 170006000
C 12	204.8	5.7	762	9 BZ604977	BZ604977 WHAAV58TR
C 13	203.8	5.7	352	1 AW089016	AW089016 xd34d02.x
C 14	203.2	5.7	656	10 AG132086	AG132086 Pan trogl
C 15	203.2	5.7	688	6 CA426034	CA426034 UI-H-DF0-
C 16	202.8	5.7	435	9 AQ542219	AQ542219 RPCI-11-3
C 17	202.4	5.6	975	5 BX331425	BX331425 BX331425
C 18	202.2	5.6	660	10 AG157820	AG157820 Pan trogl
C 19	202.2	5.6	739	9 AQ035003	AQ035003 CIT-HSP-2
C 20	202	5.6	478	1 AI627168	AI627168 ty60a05.x
C 21	201.8	5.6	513	9 AQ418548	AQ418548 RPCI-11-2
C 22	201.8	5.6	782	2 BG743198	BG743198 602634360

23	201.6	5.6	449	9 AQ769842	AQ769842 HS_3170_B
24	201.4	5.6	628	3 BM716611	BM716611 UI-B-DX1-
C 25	201	5.6	602	7 CK430039	CK430039 oJ44c10.Y
C 26	201	5.6	614	5 BX955105	BX955105 DKFZp781J
C 27	201	5.6	698	11 CR961075	CR961075 Homo sapi
C 28	200.8	5.6	681	9 AQ543621	AQ543621 RPCI-11-3
C 29	200.6	5.6	808	2 BG432758	BG432758 602496155
C 30	200.6	5.6	7845	4 CR933618	CR933618 Homo sapi
C 31	200.4	5.6	438	5 BX956646	BX956646 DKFZp781F
C 32	200.4	5.6	644	7 CN301689	CN301689 170004553
C 33	200.4	5.6	925	5 BQ433470	BQ433470 AGENCOURT
C 34	200.2	5.6	852	5 BQ690945	BQ690945 AGENCOURT
C 35	200	5.6	578	6 CD686133	CD686133 EST2654 h
C 36	199.8	5.6	551	9 AQ352725	AQ352725 CITBI-EI-
C 37	199.8	5.6	711	9 AQ415030	AQ415030 RPCI-11-2
C 38	199.8	5.6	917	6 CD558585	CD558585 AGENCOURT
C 39	199.6	5.6	521	9 AQ237142	AQ237142 RPCI11-65
C 40	199.6	5.6	576	6 CD652305	CD652305 AGENCOURT
C 41	199.6	5.6	15970	9 AQ839852	AQ839852 260L13-C5
C 42	199.4	5.6	518	9 AQ412258	AQ412258 RPCI-11-1
C 43	199.4	5.6	582	3 BP261202	BP261202 BP261202
C 44	199.4	5.6	673	3 BM728941	BM728941 UI-B-E01-
C 45	199.4	5.6	690	7 CN301690	CN301690 170005313

ALIGNMENTS

RESULT 1
AQ838273/c
LOCUS
DEFINITION
HS_4712_A2_H05_SP6R_CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=4712 Col=10 Row=O, genomic survey sequence.

ACCESSION
AQ838273
VERSION
GSS.
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Homo sapiens
Bukaryota; Metazoa; Chordata; Cnaniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS
1 (bases 1 to 549)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.

TITLE
JOURNAL
PUBMED
COMMENT
Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
10449764

Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 4712 row: O column: 10
Seq primer: T7
Classes: BAC ends
High quality sequence stop: 549.

FEATURES

source
1..549
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=4712 Col=10 Row=O"
/sex="male"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"

[illegible][illegible]

Db	122	GCCTCCCAAGTTCAAGCGAATTCCTCCTGCTCAGCCCTCTGAAGTAGCTGGGACTACAGGCA	181
Oy	1230	TGCGCCACCATTGCCCTTGCTAAATTTCTTAATTTTTTGTAGAATAGATCTCACTATAATTG	1289
Db	182	CCTGCCACCACACCAAGCTAAATTTTGTATTTTGTAGAGACGGGGTTTCAACCATGTG	241
Oy	1290	TCCAGGCTGCTTGAATTCCTGGGCTCAGGTAGAGCTCCCACTGGGCTCCCAAAGTA	1349
Db	242	GCCAGGCTGCTTGAATTCCTGAACCTCAGGTAATCCAACCTGGCTTGCCCTGAAGTG	301
Oy	1350	CTGGGATTACAGGCATGAGCCAAAGTCCCCTGCCCATATGAGATTTCTGTCTGATCC	1409
Db	302	CTGAGATTACAGGCATGAGCTGTGTGCCCCAGCCCTATTAATGATTTCTTACTGAGCA	361
Oy	1410	CATGCAGCTAGTAAATCAAGGACT	1432
Db	362	TACCAATCTCTTCTTCAATGACT	384
RESULT 9	BZ772437/c	686 bp	DNA linear GSS 13-MAR-2003
LOCUS	BZ772437	mcv36f03.g1 HFOSMID007 Homo sapiens genomic, genomic survey sequence.	
DEFINITION	BZ772437	BZ772437.1 GI:28946121	
ACCESSION	BZ772437	GSS.	
VERSION	BZ772437.1	Homo sapiens (human)	
KEYWORDS		Homo sapiens	
SOURCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
ORGANISM		Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;	
REFERENCE		Hominidae; Homo.	
AUTHORS		1 (bases 1 to 686)	
TITLE		Cook,L., Delehaunty,K., Fewell,G., Fulton,L., Magrini,V.,	
JOURNAL		Mardis,B., Miner,T., Nash,W., Williams,D. and Wilson,R.K.	
COMMENT		Homo sapiens Fosmid End Reads	
		Unpublished (2003)	
		Contact: Richard K. Wilson	
		Genome Sequencing Center	
		Washington University School of Medicine	
		Email: submissions@watson.wustl.edu	
		Plate: mcv36 row: f column: 03	
		Class: fosmid ends	
		High quality sequence start: 44	
		High quality sequence stop: 526.	
FEATURES		Location/Qualifiers	
source		1..686	
		/organism="Homo sapiens"	
		/mol_type="genomic DNA"	
		/db_xref="taxon:9606"	
		/clone_lib="HFOSMID007"	
		/note="Vector: pcc01fos; Site_1: Eco72I; Human whole genome fosmid library was prepared at Washington University Genome Sequencing Center. DNA was sheared for blunt-ended ligation into pcc01fos inducible vector. DNA was ordered from Coriell Cell Repository's DNA polymorphism discovery resource."	
ORIGIN			
Query Match	5.7%; Score 205.6; DB 9; Length 686;		
Best Local Similarity	80.6%; Pred. No. 4.3e-22;		
Matches	253; Conservative 0; Mismatches 59; Indels 2; Gaps 1;		
Db	1077 AATTAATTATTTATTTATTTTGTAGATGAGTCT--GGCTGTGCCCCAGGCTGGA	1134	
Oy	573 ATTTTCTCTTGTGTTTTTTTTTTTGAAGATGAGTCTCACTCTGTGTGCCAGGCTGA	514	
Db	1135 GTGCAGCGGGCGTGATCACAGTTCACTGCAGCGCTCAACCTTTAGGCTCAAGGATTCTCC	1194	
Oy	513 GTGCAGTGGTGTGATCTCAGCTCACTGCACCCCTCCACCTCCAGGTTCAAGTGAATTC	454	
Db	1195 CACCTCAGCCCCCAAGTAGTTGGAGCCACACGATATGCGCCACATGCTGCTAATTC	1254	
Oy			

[illegible]

Db	129	CTGGGTTCAAGTGAATTCCTCCTGCTCAGCCTCCCGAGTAGCTGGATTACAGGCATGTC	188
QY	1235	CACCATGCCCTGGCTAAATTTCTAATTTTTTTGTAGAGATGAGATCTCACTATATTTGTCCAG	1294
Db	189	CACCATGCCCTGGCTAAATTTTGTATTTTAAATAGACAGGGTTTCACCATGTTGGCAG	248
QY	1295	GCTGCTTTGAATTCCTGGGCTCAGGTYGAGCCTCCCACTGGGCTCCCAAGTACTGGG	1354
Db	249	GCTGTTCTCAAACTCCTGACCTCAAGTGAATCTGCCCACTCGGGCTCCCAAAATGTTGGG	308
QY	1355	ATTACAGGCATGAGCCAAAGTCCCTGCCCCATATGAGATTTTCT	1398
Db	309	ATTACAGGCGTAGGCCACTGCGCCTGGCCCTGTAGGCTTTTTT	352

RESULT 11

LOCUS	CN274852	533 bp	mRNA	linear	EST 16-MAY-2004
DEFINITION	170006000044196 GRN_PRENPU Homo sapiens cDNA 5', mRNA sequence.				
ACCESSION	CN274852				
VERSION	CN274852.1	GI:47291266			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				

REFERENCE	1 (bases 1 to 533)
AUTHORS	Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Risk, G.J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R., Lebkowski, J and Stanton, L.W.
TITLE	Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation
JOURNAL	Nat. Biotechnol. 22 (6), 707-716 (2004)
PUBMED	15146197
COMMENT	Contact: Brandenberger R

FEATURES

Source

Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 533 StdError: 0.00.

ORIGIN

Query Match	5.7%;	Score 204.8;	DB 7;	Length 533;
Best Local Similarity	73.9%;	Pred. No. 6.1e-22;		
Matches 260;	Conservative 0;	Mismatches 92;	Indels 0;	Gaps 0;

QY	1045	AACCATATCAGGTTTAAATTTTAAATTTTAATTAATTAATTAATTAATTTTGG	1104
Db	1	AGCCATTAGAGATTTTTAAGTATTAATTTTAAATTAATTAATTAATTTGAG	60
QY	1105	AGATGAGTCTGCGCTGCGCCCAAGCTGAGTGACAGCGCGCGATCACAGTTCACTGCAG	1164
Db	61	ACAGAGTCTCACTCTGTGCGCCCAAGCTGAGTACAGTGGTGTGATCTTGGCTCACTGCA	120
QY	1165	CCTCAACCTTCTAGGCTCAAGGSAATTCTCCCACTCAGGCCCCCAAGTAGTTGGGACCAC	1224
Db	121	CCTCCGCCCCCAGGTTCAAGGGAATTCTGTGCCCTGAGCTCCCTAGTAGCTGGAATTAC	180

QY 1225 ACGTATGCGCCACCATTGCCTGGCTAATTTCTTAATTTTTTTGTAGATAGGATCTCACTA 1284
| | | | | | | | | | | | | | | | | | | | |
Db 181 AGGCAACTGCCCACCTGCACTGGCTAATTTTGTAATTTTTTAGTAGAGACAAGGTTTCACCA 240

QY 1285 TATTGTCCAGGCTGGTCTGAATTCCTGGGCTCAGGTAGCCTCCACCTGGGCTCCCA 1344
| | | | | | | | | | | | | | | | | | | | |
Db 241 TGTTGGCAGGCTGGTCTTCACTCCTGACCTCAGGTGATCCACCACCTCGGCTGCCA 300

QY 1345 AAGTACTGGGATTACAGCATGAGCCAAAGTCCCCCTGCCCATATGAGATTTT 1396
| | | | | | | | | | | | | | | | | | | | |
Db 301 AAGTCTGGGATTACAGGTGTGAGCCACCATGCTCGGCCCAAGTTATTTT 352

RESULT 12

LOCUS	BZ604977	762 bp	DNA	linear	GSS 08-JUN-2003
DEFINITION	WHA58TR Human MCF7 breast cancer cell line library (MCF7_1) Homo sapiens genomic clone MCF7_1-6120, genomic survey sequence.				
ACCESSION	BZ604977				
VERSION	BZ604977.1	GI:31513534			
KEYWORDS	GSS.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				

REFERENCE	1 (bases 1 to 762)
AUTHORS	Volik,S., Zhao,S., Chin,K., Brebner,J.H., Herndon,D.R., Tao,Q., Kowbel,D., Huang,G., Lapuk,A., Kuo,W.-L., Magrane,G., de Jong,P., Gray,J.W. and Collins,C.
TITLE	End-sequence profiling: Sequence-based analysis of aberrant genomes
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 100 (13), 7696-7701 (2003)
PUBMED	12788976
COMMENT	Contact: Volik SV

FEATURES

Bounce

Colin Collins' lab
UCSF Comprehensive Cancer Center
UCSF Box 0808, San Francisco, CA 94143-0808, USA
Tel: 415 502 7066
Fax: 415 502 5665
Email: svollik@cc.ucsf.edu
This clone is available from Amplicon Express
<http://www.genomex.com>
Class: BAC ends.

ORIGIN

Query Match	5.74;	Score 204;	DB 9;	Length 762;
Best Local Similarity	74.18;	Pred. No. 7.5e-22;		
Matches 258; Conservative	0;	Mismatches 90;	Indels 0;	Gaps 0;

[illegible]

Db 583 AACCTCCAGGCCCAAGCAATCCGCCAATTCAGCCTCCCAAGTAGCTTGACCACAGGC 524

Qy 1229 ATGGCCCAACCATGCTGCTAATTTCTATTATTTTGTAGAGATAGATCTCACTATATT 1288
|||||

Db 523 ATGTGCCACCATGCTGCTAATTTTGTATTATTTTGTAGAGATGGGTTCACTATGCT 464

Qy 1289 GTCCAGGCTGCTTGAATTCCTGGGCTCAGGTGAGCCTCCCACTGGGCTCCCAAGT 1348
|||||

Db 463 GCCCAGGCTGCTCAAACTCCTGGGCTCAGGCCATCTATCCACTTAGCTTCCCAAGT 404

Qy 1349 ACTGGATTACAGGCATGAGCCAGGTCCCTGCCCATATGAGATT 1396
|||||

Db 403 GCTGGGATTACAGGCATGAGCCACCGTACCACCCTAAACTGACTTT 356

RESULT 13
AM089016/c 352 bp mRNA linear EST 15-OCT-1999
LOCUS
DEFINITION
xd34d02.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2595651 3',
similar to contains Alu repetitive element; contains element HGR
repetitive element ; , mRNA sequence.

ACCESSION
AM089016 GI:6044851

VERSION
AM089016.1 GI:6044851

KEYWORDS
EST.

SOURCE
Homo sapiens (human)

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 352)

REFERENCE
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

AUTHORS
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL
Unpublished (1997)

COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
www-bio.lnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 321.

FEATURES
source
1. .352
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2595651"
/tissue_type="tumor, 5 pooled (see description)"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Ov23"
/note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.35 kb. Tumor types include: mixed
Mullerian tumor, papillary serous, clear cell, spindle
cell. All are primary tumors, metastasis positive. Life
Technologies catalog #: 11534-013"

ORIGIN
Query Match 5.7%; Score 203.8; DB 1; Length 352;
Best Local Similarity 76.5%; Pred. No. 9.7e-22;
Matches 250; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

Qy 1072 TTTTAAATTATTATTATTATTATTTTGTAGATGAGTCTGGCTGCGCCAGGCT 1131
|||||

Db 337 TAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 278
|||||

Qy 1132 GGAATGACGGCGGTGATCACAGTTCAGCTCAACCTTCAAGGCTCAAGGATTC 1191
|||||

Db 277 GAGTGCAGTGGCAGATCTGGGCTCACTACAACCTTGCTCTTGGGTTCAAGTGAATC 218

Qy 1192 TCCCACTCAGCCCCCAGTAGTTGGAGCACACGTAAGCCACCATGCTGGCTAAT 1251
|||||

Db 217 TCCCACTCAGCCTCCTGAGTAGCTGGGATTACAGGCAAGCCACGACTCCTGGCTAAT 158

Qy 1252 TTCTATTATTTTGTAGAGATAGGATCTCACTATATTGTCCAGGCTGCTTGAATTCCT 1311
|||||

Db 157 TTTGTATTATTTAGTAGAGATGGGGTTTCAACCATGTTGACCAAGCTGCTTGAATACCT 98

Qy 1312 GGGCTCAGGTGAGCCTCCCACTGGGCTCCCAAGTAGCTGGGATTACAGGCATGAGCCA 1371
|||||

Db 97 GACTCAGGTGATCCACCACCTTGCCCTCCCAAGTCTGGGATTACAGGCATGAGCCA 38

Qy 1372 AGGTCCCTGCCCATATAGATTTCCT 1398
|||||

Db 37 CTGTGCCCGGCTCATTTTCTTTTCTT 11

RESULT 14
AG132086 656 bp DNA linear GSS 04-NOV-2001
LOCUS
DEFINITION
Pan troglodytes DNA, clone: PTB-144F15.R, genomic survey sequence.

ACCESSION
AG132086

VERSION
AG132086.1 GI:16661764

KEYWORDS
GSS.

SOURCE
Pan troglodytes (chimpanzee)

ORGANISM
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Pan.
1

REFERENCE
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of library PTB
Unpublished
2 (bases 1 to 656)

AUTHORS
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission

JOURNAL
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail: chimbes@gsc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/
Tel: 81-45-503-9111, Fax: 81-45-503-9170)

COMMENT
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the Rad process and may have higher chance of
clone tracking errors.

PRIMERS
Sequencing: M13Rev

LIBRARY
Vector : PKS145
R.Site 1 : SacI
R.Site 2 : SacI.

FEATURES
source
1. .656
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-144F15.R"
/sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"

ORIGIN
Query Match 5.7%; Score 203.2; DB 10; Length 656;
Best Local Similarity 77.5%; Pred. No. 1e-21;
Matches 259; Conservative 0; Mismatches 73; Indels 2; Gaps 1;

Qy 1060 TTAATTTTAAATTAAATTAATTAATTAATTAATTAATTTTGTAGATGAGTCTGG-- 1117
|||||

Db 73 TAAGTATTTGACGCTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 132
|||||

QY	1118	CTGTGCGCCAGGCTGGAGTGCAGCGGCGTGATCACAGTTCACTGCAGCCTCAACCTTCTA	1177
Db	133	CTGTGCGCCAGGCTGGAGTGCAGTGCAGCCATCTCGGCTCACTGCACCTCCACTTCTTG	192
QY	1178	GGCTCAAGGGATTCTCCCACTCAGCCCCCAAGTAGTTGGAGCCACACGTAATGCGCAC	1237
Db	193	GGTTCAGCGATTATCTGCTCAGCCTCCTGAGTAGTTGGAGATTACAGGCACCTGCGCAC	252
QY	1238	CATGCCCTGGCTAATTTCTAATTTTTGTAGAGATAGATCTCATATATGTGCCAGCT	1297
Db	253	CATGCCCAGCTAATTTTCTAATTTTTAGTAGAGACGGGGTTCAACATGTTGTTCAAGCT	312
QY	1298	GGTCTTGAATTCCTGGGCTCAGGTGAGCCTCCCACTGGGCTCCCAAGTACTGGGATT	1357
Db	313	GGCTTGAACCTCTGACCTCAGGTGATCCACCCGCTTGCTCTCCCAAGTGTGGGATT	372
QY	1358	ACAGGCATGAGCCCAAGGTCCCTGCCCCATATGAG	1391
Db	373	ACAGGCATGAGCCCAACCATGCCCCAGCCTATATTAG	406

RESULT 15	CA426034	LOCUS	CA426034	688 bp	mRNA	linear	EST 07-NOV-2002
DEFINITION	UI-H-DP0-bej-o-13-0-UI.s1		NCI CGAP DP0 Homo sapiens				CDNA clone
	UI-H-DP0-bej-o-13-0-UI 3'		mRNA sequence.				

ACCESSION	CA426034	GI:247887600
VERSION	CA426034.1	
KEYWORDS	EST.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 688)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.

Email: cgagbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@iowa.edu
The following repetitive elements were found in this cDNA
sequence: 1-48, >POLY_A#Simple_repeat (matched complement) 50-337,
>ALU (matched complement)
Seq primer: M13 FORWARD
POLYA=yes.

FEATURES	Location/Qualifiers
source	1. .688

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="JI-H-DF0-bej-o-13-0-UI"
/tissue_type="Subchondral Bone"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_1lb="NCI_CGAP_DF0"
/note="Organ: Bone; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
NCI CGAP DF0 is a cDNA library containing the following
tissue(s): Subchondral Bone. The library was constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pT7T3-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is

```

located between the Not I site and the (dT)₁₈ tail. The sequence tag for this library is GTTAAGCGTC.
TAG_TISSUE=subchondral bone
TAG_LIB=UI-H-DP0
TAG_SEQ=GTTAAGCGTC"

Query Match	5.7%;	Score 203.2;	DB 6;	Length 688;
Best Local Similarity	78.1%;	Pred. No. 1e-21;		
Matches 257, Conservative	0;	Mismatches 70;	Indels 2;	Gaps 1;

[illegible]

Search completed: January 7, 2006, 19:14:08
Job time : 13089.4 secs

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located between the Not I site and the (dT)18 tail. The
sequence tag for this library is GTTAAGCGTC.
TAG_TISSUE=subchondral bone
TAG_LIB=UI-H-DP0
TAG_SEQ=GTTAAGCGTC"
ORIGIN

Query Match      5.7%; Score 203.2; DB 6; Length 688;
Best Local Similarity 78.1%; Pred. No. 1e-21;
Matches 257; Conservative 0; Mismatches 70; Indels 2; Gaps 1;

QY      1057 TTTTAAATTTTTAAATTTTAAATTATTTATTTATTTATTTGAGATGAGTCTG 1116
Db       9   TTTTCTTCTTATTTATTTATTTATTTATTTATTTATTTATTTTGACAGGGGTCTT 68

QY      1117 G--CTGTGCCCAAGCTGAGTGCAGCGCGGTGATCACAGTTCACTGCAGCCTCAACCCTT 1174
Db       69 TATCTGTGCCCTGGCTGAGTGCAGTGTGCATCATAGCCCACTGCAGCCTCGAACCTC 128

QY      1175 CTAGGCTCAAGGAATTCCTCCACCTCAGCCCCCCCAAGTAGTGTGGACCAAGTATGCCG 1234
Db       129 CTAGGCTTAAGTATCTCCACCTCAGCCTCCCAAAGTAGCTGGACCAAGGTATTT 188

QY      1235 CACCATGCGTGGCTAATTTCTTATTTTGTAGAGATAGGATCTCACTATATTGTCCAG 1294
Db       189 CACCATGCCAGCTAATTTTGTATTTTGTAGAGATGGGGTTTGCCAATGTGCCCTAG 248

QY      1295 GCTGTCTTGAATTCCTGGGCTCAGGTGAGCCTCCCACTGGGCTCCCAAAGTACTGGG 1354
Db       249 GCTGTCTTGAATTCCTGGAATCAGGAGATCTGCCCACTCAGCCTCCCAAAGTGTGG 308

QY      1355 ATTACAGGCATGAGCCAAGTCCCCTGCC 1383
Db       309 ATTACAAGCATAGCCACTGTGCCAGGCC 337

Search completed: January 7, 2006, 19:14:08
Job time : 13089.4 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 7, 2006, 03:54:36 ; Search time 1957.21 Seconds
(without alignments)
12211.020 Million cell updates/sec

Title: US-10-767-521-3
Perfect score: 3586
Sequence: 1 ggatccctaccttcccatc.....ctatcacaggagaagtga 3586

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 segs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_21:*
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3: geneseqn2000s:*
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12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	3586	100.0	5099	2	AAT93601	Aat93601 Human eos
2	3494.4	97.4	5791	8	ABZ68879	Abz68879 Nucleotid
3	3494.4	97.4	5791	14	ADY86631	Ady86631 Human CC
4	2406	67.1	7201	6	ABL32337	Ab132337 Human imm
5	2271.8	63.4	7201	6	ABL32336	Ab132336 Human imm
6	344.2	9.6	1915	2	AAT85162	Aat85162 Human che
7	344.2	9.6	1915	10	ADC03342	Adc03342 Human CDN
8	344.2	9.6	1915	13	ADT90848	Adt90848 Human che
9	344.2	9.6	1915	13	ADU47727	Adu47727 Human che
10	211.8	5.9	54701	11	ACN44478	Acn44478 Human gen
11	210.6	5.9	102790	13	ABD32649	Abd32649 Human can
12	210.6	5.9	160361	12	ADL08116	Adl08116 Human gen
13	210.2	5.9	168821	11	ACN44262	Acn44262 Human gen
14	210	5.9	1215	6	ABV76540	Abv76540 Human pro
15	209.8	5.9	10554	8	ABZ74119	Abz74119 Secreted
16	209.8	5.9	10554	10	ABZ67679	Abz67679 Human sec
17	209.8	5.9	10558	8	ABZ74118	Abz74118 Secreted
18	209.8	5.9	10558	10	ABZ67678	Abz67678 Human sec
19	209	5.8	3660	5	ABA17973	Abal7973 Human ner

C	20	209	5.8	3662	5	ABA17972	Abal7972 Human ner
C	21	209	5.8	59215	8	AAD36834	Aad36834 Human tra
C	22	209	5.8	173805	10	ADL13775	Adl13775 Osteoarth
C	23	208.8	5.8	171158	12	ADQ97894	Adq97894 Human can
C	24	208.2	5.8	235033	2	AAV57926	Aav57926 Hereditar
C	25	207.8	5.8	295772	12	ADQ97433	Adq97433 Human can
C	26	206.4	5.8	110000	12	ADQ34435_2	Adq34435 Human can
C	27	206.4	5.8	119501	12	ADT29095	Adt29095 Human MAR
C	28	206.2	5.8	11901	2	AAK02998	Aak02998 Human IL-
C	29	206.2	5.8	42299	4	AAK68932	Aak68932 Human imm
C	30	206.2	5.8	62658	13	ABD33339	Abd33339 Human can
C	31	206.2	5.8	101433	14	ABZ61169_3	Abz61169 Human can
C	32	206	5.7	3324	13	ADR08168	Adr08168 Full leng
C	33	206	5.7	3417	4	AAH18467	Aah18467 Human CDN
C	34	206	5.7	108316	10	ADC87336	Adc87336 Human GPC
C	35	205.6	5.7	73967	11	ACN44438	Acn44438 Human gen
C	36	205.6	5.7	186739	12	ADK43195	Adk43195 Human pro
C	37	205.4	5.7	1273	5	ABA21094	Aba21094 Human ner
C	38	205.4	5.7	177380	8	ACF62751	Acf62751 Cancer ba
C	39	205.4	5.7	177380	8	ADB20870	Adb20870 MRP1 base
C	40	205.4	5.7	177380	10	ADB87959	Adb87959 Human UGT
C	41	205.4	5.7	177380	10	ADB96942	Adb96942 Human MDR
C	42	205.4	5.7	177380	10	ADB92133	Adb92133 Human MDR
C	43	205	5.7	1376	3	AAC99845	Aac99845 Human sec
C	44	205	5.7	10800	4	AAK83329	Aak83329 Human imm
C	45	205	5.7	29629	6	ABL58699	Ab158699 Human kin

ALIGNMENTS

RESULT 1	
ID	AAT93601 standard; cDNA; 5099 BP.
AC	AAT93601;
DT	07-MAY-1998 (first entry)
DS	Human eosinophil eotaxin receptor CC CKR3 encoding cDNA.
KW	Eosinophil eotaxin receptor; CC CKR3; human; treatment; dermatitis; atopic condition; allergic rhinitis; conjunctivitis; bronchial asthma; beta-chemokine receptor; viral infection; ss.
OS	Homo sapiens.
FT	Key
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FT	location/Qualifiers
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FT	/note= "5' genomic DNA flanking sequence"
FT	3587..4654
FT	/*tag= b
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FT	4655..5099
FT	/*tag= c
FT	/note= "terminator region"
FT	CDS
FT	WO9741154-A1.
PD	06-NOV-1997.
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PF	24-APR-1997; 97WO-US006568.
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PR	26-APR-1996; 96US-0016158P.
PR	26-APR-1996; 96US-0017113P.
PR	17-JAN-1997; 97GB-00000894.
XX	
PA	(MERCK) MERCK & CO INC.
XX	
PI	Daugherty BL, Demartino JA, Springer MS, Siciliano SJ;
XX	
DR	WPI; 1997-549685/50.

DR P-PSDB; AAW31850.
XX
PT New isolated human eosinophil eotaxin receptor - used to develop products
PT for treating and preventing atopic conditions e.g. allergic rhinitis,
PT dermatitis, conjunctivitis and bronchial asthma.
XX
PS Claim 12, 13, 14; Page 16-20; S1pp; English.
XX
CC This cDNA encodes a human eosinophil eotaxin receptor. This 5099 base
CC pair sequence comprises a 1065 base pair open reading frame encoding a
CC 355 amino acid eosinophil eotaxin receptor protein, flanked by a 5'
CC genomic DNA sequence and a 3' terminator region. This novel eosinophil
CC eotaxin receptor is a human beta-chemokine receptor designated CC CKR3.
CC Agents which bind to this eosinophil eotaxin receptor can be used for the
CC treatment and prevention of atopic conditions such as allergic rhinitis,
CC dermatitis, conjunctivitis and bronchial asthma. Agents which block this
CC eosinophil eotaxin receptor can be used to prevent viral infection in
CC healthy individuals and slow or halt viral progression in infected
CC patients
XX
SQ Sequence 5099 BF, 1388 A; 1171 C; 1013 G; 1527 T; 0 U; 0 Other;

Query Match 100.0%; Score 3586; DB 2; Length 5099;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3586; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 CCCCAGGAATGTCTCCCTGTGGGCACTTCTTACCAGATGGATGGCCAGTGGGTT 120
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DB 121 AAGTTGGTGTGTCAGGCAAGAAAAAAGATCTAGTTGTACTCTTGAGAGTTCCCGTTT 180
QY 181 GTTCATGGCATGGGCAAGGAGTCAAGAGCAGCAGCTTGCTCAGTGCCTACCAAGTGA 240
DB 181 GTTCATGGCATGGGCAAGGAGTCAAGAGCAGCAGCTTGCTCAGTGCCTACCAAGTGA 240
QY 241 GGAAGAGGTGCATAGCCTGGGCGCAGGGCCCTGTGTGAGGCGTATGTGTAACAGA 300
DB 241 GGAAGAGGTGCATAGCCTGGGCGCAGGGCCCTGTGTGAGGCGTATGTGTAACAGA 300
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DB 301 GAGGGCTCTCCATTCCAGCCCCAAGGAGACTAAGATGAATACCTCATGATATATTAGC 360
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DB 361 TACAAACCAACACAGCAGGTTCCAGAAAAAGGCTCAGCGTTGAAACAGGTCACCCCAC 420
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DB 601 ACCTAAATCATTTGTTTCAATGAATGAATCAAGAGAAGTTTAAACACTTTGACTAAA 660
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DB 661 TGTGTGAATCCTTTTCTCTGCTATCCAGAGATGAAGAAGCTGTAAACAGACCAATA 720

QY 721 GTTTGAGACTAAAGAAATCATTGCAATTTCACTGCTGAGTTGTATTGTGATATTTTA 780
DB 721 GTTTGAGACTAAAGAAATCATTGCAATTTCACTGCTGAGTTGTATTGTGATATTTTA 780
QY 781 GTTGACCTCACTTTGTTAAATCTTGACACACGGGGCAATCCAATATCTGCACAAAGATATG 840
DB 781 GTTGACCTCACTTTGTTAAATCTTGACACACGGGGCAATCCAATATCTGCACAAAGATATG 840
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DB 841 TTAACCAAGTGTAATGCTGCATGAGAGATTTGGTGAATTTTACTTTCGTTTTGTGCT 900
QY 901 CTTCCTTCTTATTTGTCTTACTTATTTACGATTAACCTATTCGTTTCCCAAAATGTA 960
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DB 961 GGCCATTTTGAAAGCCTTAATTCAAACCTCTTCACTAATTTTGATCTAAGTATTCACCTTG 1020
QY 1021 ATTGAGACTGGGTAGACAGGTGAAACCATATCAGGTTTAAATTTTAAATTTTAAAT 1080
DB 1021 ATTGAGACTGGGTAGACAGGTGAAACCATATCAGGTTTAAATTTTAAATTTTAAAT 1080
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DB 1081 ATTTATTTATTTATTTATTTTGTAGATGAGTCTGGCTGTCCGCCAGGCTGAGTGACAG 1140
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DB 1681 TTAACGGTGAATACAGGCTACTATACTTGTCTCCAGAAATTAAGCAATCTGTTCTTTT 1740
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QY 1921 ATGTGCCATTGATCAGTGGAGATGTAAGTGAAGTGAAGAGATCAACAAAGT 1980
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QY 3541 CATTTGGGATTTGATTTTCTTCTTCTATACAGGAGAGATGAA 3586
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RESULT 2
ABZ68879
ID ABZ68879 standard; cDNA; 5791 BP.
XX
XX AC ABZ68879;
XX
XX DT 28-MAY-2003 (first entry)
XX
DE Nucleotide sequence of human chemokine receptor CCR3.
XX
KW Human; chemokine receptor; CCR3; viral infection; surface protein;
KW respiratory virus infection; respiratory syncytial virus infection;
KW RSV infection; bronchiolitis; bronchitis; pneumonia; asthma; gene; ss.
XX
OS Homo sapiens.
XX
FH Key location/Qualifiers
FH CDS 4015..5082
FH FT /*tag= a
FH FT /product= "CCR3"
PN WO2003014153-A2.
XX
PD 20-FEB-2003.
XX
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PF 12-AUG-2002; 2002WO-CA001248.
XX
PR 10-AUG-2001; 2001US-0311088P.
XX
PA (TOPI-) TOPIGEN PHARM INC.
XX
PI Renzi P, Zenzoumi K;
XX
DR WPI; 2003-256541/25.
DR P-PSDB; ABP97726.

XX
PT Modulating viral infection of a cell, for treating or preventing
PT respiratory virus infections, bronchitis, pneumonia or asthma, by
PT modulating a binding interaction between a cell chemokine-receptor and a
PT surface protein of the virus.
XX

PS Disclosure; Page 84-88; 120pp; English.

XX
CC The present sequence encodes human chemokine receptor CCR3. The
CC specification describes a method for modulating viral infection of a
CC cell. the method comprises modulating a binding interaction between a
CC cell chemokine-receptor and a surface protein of the virus. The proviso
CC is that the cell chemokine-receptor is not CX3CR1 and that the virus is
CC not HIV. The method is useful for treating or preventing respiratory
CC virus infection in vertebrates, more particularly respiratory syncytial
CC virus (RSV) infections, and related diseases, e.g. bronchiolitis,
CC bronchitis, pneumonia or asthma
XX

SQ Sequence 5791 BF; 1624 A; 1285 C; 1160 G; 1722 T; 0 U; 0 Other;

Query Match 97.4%; Score 3494.4; DB 8; Length 5791;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 3569; Conservative 0; Mismatches 11; Indels 8; Gaps 6;

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QY 61 CCCCAGGAATGTCTCCCTGTGGGCACTTCTTACCAGATGGGATGGCAGTGGGTT 120
DB 493 CCCCAGGAATGTCTCCCTGTGGGCACTTCTTACCAGATGGGATGGCAGTGGGTT 552
QY 121 AAGTTGTGTGTCAGGCAGAAAAAAGATCTAGTTGTACTCTTGAGAGTTCCCGGTT 180
DB 553 AAGTTGTGTGTCAGGCAGAAAAAAGATCTAGTTGTACTCTTGAGAGTTCCCGGTT 612
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DB 673 GGAAGAGGTGATAGCCTGGGCGAGGGCCAGGGCCCTGTGGAGCGTAGTGTAAACA 732
QY 301 GAGGCTCTCCATTCAGCCCAAGGAAGCTAAGATGAATACCTCATGATATATTAGC 360
DB 733 GAGGCTCTCCATTCAGCCCAAGGAAGCTAAGATGAATACCTCATGATATATTAGC 792
QY 361 TACAAACCAACACAGCAGGTTCCAGAAAAAGGCTCAGCGTTGGAACCAAGTCACCCCAC 420
DB 793 TACAAACCAACACAGCAGGTTCCAGAAAAAGGCTCAGCGTTGGAACCAAGTCACCCCAC 852
QY 421 TCAGCAGACACCAAGTCAATATAATCAAGAGCAACCAAGAGACAGAACACCCCTTCCA 480
DB 853 TCAGCAGACACCAAGTCAATATAATCAAGAGCAACCAAGAGACAGAACACCCCTTCCA 912
QY 481 CTCGCCCATGTCTCAAGTTGTAGGCGCTTCTCCAGATCTGTGCCACCATCTTAGA 540
DB 913 CTCGCCCATGTCTCAAGTTGTAGGCGCTTCTCCAGATCTGTGCCACCATCTTAGA 972
QY 541 AAGGAACACTGAAGAAGAACTGAATTATAAGCTGACAGCATAAAGAGATGAGTAA 600
DB 973 AAGGAACACTGAAGAAGAACTGAATTATAAGCTGACAGCATAAAGAGATGAGTAA 1032

QY 601 ACCTAAATCATTTGTTCAATGAATGAATCAAGAGAGTTTAAACCACTTTGACTAAA 660
DB 1033 ACCTAAATCATTTGTTCAATGAATGAATGAATCAAGAGAGTTTAAACCACTTTGACTAAA 1092
QY 661 TGTGTGAATCCTTTTCTGCTATCCAGCAGATGAGAACTGTGTACAGAGACCAATA 720
DB 1093 TGTGTGAATCCTTTTCTGCTATCCAGCAGATGAGAACTGTGTACAGAGACCAATA 1152
QY 721 GTTGGAGACTAAAGATCAATGCAATTTCACTGCTGAGTGTATTGTGAGTAATTTA 780
DB 1153 GTTGGAGACTAAAGATCAATGCAATTTCACTGCTGAGTGTATTGTGAGTAATTTA 1212
QY 781 GTTGACCTCAC-TTTGTAATCTTGACACAGGGGCAATCCAATATCTGACAGAATAT 839
DB 1213 GTTGACCTCAC-TTTGTAATCTTGACACAGGGG--CATCCATATCTGCAC-AGAGATAT 1268
QY 840 GTTAACCACTGTAAATGCTGCATGAGAGATTTGGGTGATTTTACTTTGTTTGTGC 899
DB 1269 GTTAA-CAGTGTAAATGCTGCATGAGAGATTTGGGTGATTTTACTTTGTTTGTGC 1327
QY 900 TCTTCTTCTTATTTGTTCTTACTTATTTAGATTAACCTATGCTTTCCCAATGTAAA 959
DB 1328 TCTTCTTCTTATTTGTTCTTACTTATTTAGATTAACCTATGCTTTCCCAATGTAAA 1386
QY 960 AGGCCATTTGAAAGCCTAATTCAAACCTCTTCACTATTTTGTATCTAAGATCACTT 1019
DB 1387 AGGCCATTTGAAAGCCTAATTCAAACCTCTTCACTATTTTGTATCTAAGATCACTT 1446
QY 1020 GATTGAGACTGGGTAGACAGGTGAAAAACCAATATCAGGTTTAAATTTTAAATTTTAAAT 1079
DB 1447 GATTGAGACTGGGTAGACAGGTGAAAAACCAATATCAGGTTTAAATTTTAAATTTTAAAT 1506
QY 1080 TATTTATTTATTTATTTATTTTGTGAGATGAGTCTGCTGCGCCAGGCTGAGTGCA 1139
DB 1507 TATTTATTTATTTATTTATTTTGTGAGATGAGTCTGCTGCGCCAGGCTGAGTGCA 1566
QY 1140 GCGGCGTGATCACAGTTCACTGCAAGCCTCAACCTTTAGGCTCAAGGATTTCTCCACT 1199
DB 1567 GCGGCGTGATCACAGTTCACTGCAAGCCTCAACCTTTAGGCTCAAGGATTTCTCCACT 1626
QY 1200 CAGCCCCCAAGTATGTTGGACCAACAGTATGCGGCCACCATGCTGCTAATTTCTTAAT 1259
DB 1627 CAGCCCCCAAGTATGTTGGACCAACAGTATGCGGCCACCATGCTGCTAATTTCTTAAT 1686
QY 1260 TTTTGTAGAGATAGATCTCACTATATTGTCCAGGCTGCTGTAATTCCTGGGCTCAG 1319
DB 1687 TTTTGTAGAGATAGATCTCACTATATTGTCCAGGCTGCTGTAATTCCTGGGCTCAG 1746
QY 1320 GTGAGCTCCACCTGGGCTCCCAAGTACTGGGATTAACAGCATGAGCCAAAGTCCCC 1379
DB 1747 GTGAGCTCCACCTGGGCTCCCAAGTACTGGGATTAACAGCATGAGCCAAAGTCCCC 1806
QY 1380 TGCCCATATGAGATTTTCTGTCTCTGATCCATGCAAGTGAATCAAGGACTTGCTGC 1439
DB 1807 TGCCCATATGAGATTTTCTGTCTCTGATCCATGCAAGTGAATCAAGGACTTGCTGC 1866
QY 1440 TGACTCTGAGGACCTGCAATGCTTTCTTGAGCTGTGAACCTTCAAGTCAAAAGCTCATAG 1499
DB 1867 TGACTCTGAGGACCTGCAATGCTTTCTTGAGCTGTGAACCTTCAAGTCAAAAGCTCATAG 1926
QY 1500 GCAAGCTTGAACCCCAACCAAAAGGTTCTATGTTATCATCTGATCATGTTGATTTT 1559
DB 1927 GCAAGCTTGAACCCCAACCAAAAGGTTCTATGTTATCATCTGATCATGTTGATTTT 1986
QY 1560 ATGAATAAACAATGAATTAAGACATACCTCAAACTGAGCAAAACTTAAGTAATTT 1619
DB 1987 ATGAATAAACAATGAATTAAGACATACCTCAAACTGAGCAAAACTTAAGTAATTT 2046
QY 1620 TTTTAAAGTTGACCTGTTTAAATCACTCTTGAGAGAAAAAGAAATTAATACAATA 1679
DB 2047 TTTTAAAGTTGACCTGTTTAAATCACTCTTGAGAGAAAAAGAAATTAATACAATA 2106

Qy	1680	ATTAA	CGGTGA	ATACAG	GGTACTAT	ATACCTT	GTGTTCTCC	AGAA	TTAGCAG	TTCTGTCTTT	1739			
Db	2107	ATTAA	CGGTGA	ATACAG	GGTACTAT	ATACCTT	GTGTTCTCC	AGAA	TTAGCAG	TTCTGTCTTT	2166			
Qy	1740	TCTTG	CTTTAG	ATGCTGA	GTGCAG	AGAGCACTCTG	TGATTGTAC	GTGTAA	CTGACA		1799			
Db	2167	TCTTG	CTTTAG	ATGCTGA	GTGCAG	AGAGCACTCTG	TGATTGTAC	GTGTAA	CTGACA		2226			
Qy	1800	AAATG	TGTA	TTTTTTT	CTCAG	CTGCTAT	GGATTGGA	TTATG	CTATTATGA	TAAGAATG	1859			
Db	2227	AAATG	TGTA	TTTTTTT	CTCAG	CTGCTAT	GGATTGGA	TTATG	CTATTATGA	TAAGAATG	2286			
Qy	1860	CTGAT	GGAGCA	CACA	CAAA	CCATTG	TTCCTCAG	TTCATT	TTCCTCCTCA	AAAAGCTGG	1919			
Db	2287	CTGAT	GGAGCA	CACA	CAAA	CCATTG	TTCCTCAG	TTCATT	TTCCTCCTCA	AAAAGCTGG	2346			
Qy	1920	AATG	TGCCAT	TGATCAG	TGGGAGAT	GTACTG	GACAGACC	TGA	AAAGAGAT	CAACAAG	1979			
Db	2347	AATG	TGCCAT	TGATCAG	TGGGAGAT	GTACTG	GACAGACC	TGA	AAAGAGAT	CAACAAG	2406			
Qy	1980	TTCCAC	CCCAAG	GGACCCTA	TTTTTCT	TAATTTCA	TTTGA	ATGGCT	CTAAT	TGTCTTC	2039			
Db	2407	TTCCAC	CCCAAG	GGACCCTA	TTTTTCT	TAATTTCA	TTTGA	ATGGCT	CTAAT	TGTCTTC	2466			
Qy	2040	TTTCAT	TCCGTG	CTTCTAC	CAAGTTT	TACAGCT	TTTTCTG	TTTCA	ATGTGA	ACTCACA	2099			
Db	2467	TTTCAT	TCCGTG	CTTCTAC	CAAGTTT	TACAGCT	TTTTCTG	TTTCA	ATGTGA	ACTCACA	2526			
Qy	2100	AACT	CTCAT	TTTTTCC	TATCA	CAACCC	CAAGTGA	CCCAATG	GTCTCA	TTTGCATATA	2159			
Db	2527	AACT	CTCAT	TTTTTCC	TATCA	CAACCC	CAAGTGA	CCCAATG	GTCTCA	TTTGCATATA	2586			
Qy	2160	AGTA	AAAGAG	GGCTCTG	CA	TTAAAG	GGCTGTG	TCCAAG	GCACG	CTGAGAGGCGCTA	GGAC	2219		
Db	2587	AGTA	AAAGAG	GGCTCTG	CA	TTAAAG	GGCTGTG	TCCAAG	GCACG	CTGAGAGGCGCTA	GGAC	2646		
Qy	2220	TGG	CTCATT	TTCAT	CTAT	TCTCA	TGACTG	ACTTGA	CTAC	CCAGAACCCCA	CAATGTGGG	2279		
Db	2647	TGG	CTCATT	TTCAT	CTAT	TCTCA	TGACTG	ACTTGA	CTAC	CCAGAACCCCA	CAATGTGGG	2706		
Qy	2280	GCCT	CAGAT	TTCGAT	CAATTA	TCTATTA	AGAAGCA	AAACAA	TTC	CCCGCAT	TGGCCC	2339		
Db	2707	GCCT	CAGAT	TTCGAT	CAATTA	TCTATTA	AGAAGCA	AAACAA	TTC	CCCGCAT	TGGCCC	2766		
Qy	2340	AGT	TATTA	AGCAT	TTCTC	AGATTTA	CCCTTG	AGA	AAATG	CCCATCG	CGCTGTAT	TTCACAT	2399	
Db	2767	AGT	TATTA	AGCAT	TTCTC	AGATTTA	CCCTTG	AGA	AAATG	CCCATCG	CGCTGTAT	TTCACAT	2826	
Qy	2400	CTT	CACCC	TTGTCC	CTTCTCT	CTAGA	AAAGAG	AAAGTCA	GTGAT	GCCTCTG	AGAAC	2459		
Db	2827	CTT	CACCC	TTGTCC	CTTCTCT	CTAGA	AAAGAG	AAAGTCA	GTGAT	GCCTCTG	AGAAC	2886		
Qy	2460	TAG	TGAT	GGCTTA	CTGTCT	CTCAT	GACTCC	TGCTTAT	CTGTTT	CTATTT	CTCTCC	2519		
Db	2887	TAG	TGAT	GGCTTA	CTGTCT	CTCAT	GACTCC	TGCTTAT	CTGTTT	CTATTT	CTCTCC	2946		
Qy	2520	TTTT	CCACCG	AAAGTCTA	TAA	TCTCA	AGAAA	AGCAG	GCAC	TGGCCTTA	GGGCTCTG	GGCT	2579	
Db	2947	TTTT	CCACCG	AAAGTCTA	TAA	TCTCA	AGAAA	AGCAG	GCAC	TGGCCTTA	GGGCTCTG	GGCT	3006	
Qy	2580	AAGA	AATAT	CAAGTCC	AGTGA	AAATCC	CATTG	ACTGA	CCCTC	TGCTTAC	CCCTTGT	2639		
Db	3007	AAGA	AATAT	CAAGTCC	AGTGA	AAATCC	CATTG	ACTGA	CCCTC	TGCTTAC	CCCTTGT	3066		
Qy	2640	GAT	GAGA	AGCTCC	CA	GGGGTTG	CTTTTG	CA	TGTACA	GGCCTA	ACTCAG	CA	2699	
Db	3067	GAT	GAGA	AGCTCC	CA	GGGGTTG	CTTTTG	CA	TGTACA	GGCCTA	ACTCAG	CA	3126	
Qy	2700	AGGG	CGA	AGAAA	AGAA	AGTAA	CTTAA	ACTA	TGCTG	CTTATA	TGTAT	TGTAT	2759	
Db	3127	AGGG	CGA	AGAAA	AGAA	AGTAA	CTTAA	ACTA	TGCTG	CTTATA	TGTAT	TGTAT	3186	
Qy	2760	AGT	TAA	TACTG	TGAT	TGTAC	TGTGT	TAC	GACAG	CAAAATG	TGTATTTT	TTCACAG	CTGC	2819

Db	3187	AGTTAATTA	CTGTGATTTGTA	CACTGTGTAA	CAGACA	CAAAATGTGTATTTTTCACAGCTGC	3246
QY	2820	TTGTGATTTG	GAATATATGCCA	TTTGGAA	TAGAATGCTGTTA	AGAGACACAAGCCAGGTTTC	2879
Db	3247	TTGTGATTTG	ATTAATGCCATTTT	GGAA	TAAAGATGCTGTTA	AGAGACACAAGCCAGGTTTC	3306
QY	2880	CTCAAGTCCG	TAGCAAAATTTT	CAAAA	AGTTAAATTTT	AAAAATCACTACATTTGAACTAG	2939
Db	3307	CTCAAGTCCG	TAGCAAAATTTT	CAAAA	AGTTAAATTTT	AAAAATCACTACATTTGAACTAG	3366
QY	2940	TGACAGAGAA	TGACATGATAG	AGACTAA	AGATCTAGCCCAA	ATTTATATTAATTA	2999
Db	3367	TGACAGAGAA	TGACATGATAG	AGACTAA	AGATCTAGCCCAA	ATTTATATTAATTA	3426
QY	3000	GTTAGAGAT	TTTGAACAA	ATTACTAA	ATTCTTCAAGTTC	CAATTTCCCAATTA	3059
Db	3427	GTTAGAGAT	TTTGAACAA	ATTACTAA	ATTCTTCAAGTTC	CAATTTCCCAATTA	3486
QY	3060	AATGAATG	CTCATCATTA	TGSGGCGCTG	AGAGAGCATTA	TTACTTGTATTTGTAATTA	3119
Db	3487	AATGAATG	CTCATCATTA	TGSGGCGCTG	AGAGAGCATTA	TTACTTGTATTTGTAATTA	3546
QY	3120	CATTGTTAT	TATTATTATAC	ATTTTGTCTTT	TAATGATTA	AGATTTTAAAGTATAT	3179
Db	3547	CATTGTTAT	TATTATTATAC	ATTTTGTCTTT	TAATGATTA	AGATTTTAAAGTATAT	3606
QY	3180	GTAACCTG	TAAAAACATA	AAATGCAAA	ATGCGGTAA	GAGACAGTAGTAATAATGATTA	3239
Db	3607	GTAACCTG	TAAAAACATA	AAATGCAAA	ATGCGGTAA	GAGACAGTAGTAATAATGATTA	3666
QY	3240	TTATATTG	TATCATTA	TCTAGCCTG	TTTTCCTG	TGTGTAATTTCTTCCTTAAATGC	3299
Db	3667	TTATATTG	TATCATTA	TCTAGCCTG	TTTTCCTG	TGTGTAATTTCTTCCTTAAATGC	3726
QY	3300	TTACAGAA	ATCTGTATCC	CCCATTTCT	CAACCA	CCCAACAATTTCTGCTTCTTCC	3359
Db	3727	TTTACAGAA	ATCTGTATCC	CCCATTTCT	CAACCA	CCCAACAATTTCTGCTTCTTCC	3786
QY	3360	CATGCC	-GGTCATG	CTACTACTT	GAAAGCTT	CAGCTCTTCCCTCAATCCTTCCCTG	3418
Db	3787	CATGCC	-GGTCATG	CTACTACTT	GAAAGCTT	CAGCTCTTCCCTCAATCCTTCCCTG	3846
QY	3419	GCACCTCT	GATATGCTT	TGAAATTC	ATCTTTAA	AGAAATCCCTAGGCTGCTATCA	3478
Db	3847	GCACCTCT	GATATGCTT	TGAAATTC	ATCTTTAA	AGAAATCCCTAGGCTGCTATCA	3906
QY	3479	GGCATCTT	GTGATGATAC	ATGAATCA	ACTGCTGTG	TTTACGAAGGATGATTA	3538
Db	3907	GGCATCTT	GTGATGATAC	ATGAATCA	ACTGCTGTG	TTTACGAAGGATGATTA	3966
QY	3539	TTCAATG	TGGATTTGTAT	TTTCTTCTT	CTATCA	CAGGAGAGTGA	3586
Db	3967	TTCAATG	TGGATTTGTAT	TTTCTTCTT	CTATCA	CAGGAGAGTGA	4014

RESULT 3	
ADY86631	
ID	ADY86631 standard; DNA; 5791 BP.
XX	
AC	ADY86631;
XX	
DT	02-JUN-2005 (first entry)
XX	
DE	Human CC chemokine receptor 3 (CCR3) gène.
XX	
KW	Gene expression; screening; multiple sclerosis; neuroprotective;
KW	immune disorder; neurologic disease; DNA microarray; gene; ds;
KW	chemokine.
XX	
OS	Homo sapiens.
XX	
PN	US2005064483-A1.

XX 24-MAR-2005.
PD
XX 30-AUG-2004; 2004US-00929182.
PF
XX 28-AUG-2003; 2003US-0498731P.
PR
XX (BAYU) BAYLOR COLLEGE MEDICINE.
PA
XX Zang JZ, Hong J;
PI
XX WPI; 2005-252668/26.
DR
XX GENBANK; AF247361.
DR
XX
PT Monitoring multiple sclerosis patient taking beta-interferon or
PT glatiramer acetate to predict treatment response by determining
PT expression profile of inflammatory nucleic acids using RNA of patient and
PT comparing to control.
XX
XX
PS Claim 1; SEQ ID NO 21; 73pp; English.
XX
XX The present invention relates to gene expression profiling technology to
CC quantitatively measure the expression profiles of genes selected based on
CC their role in inflammation and their susceptibility to regulation by
CC current multiple sclerosis (MS) treatment agents by isolating RNA from
CC peripheral blood mononuclear cells (PBMC) of patient. The invention is
CC particularly useful for monitoring a multiple sclerosis patient taking
CC interferon-beta (IFN-beta) or glatiramer acetate (GA) in order to predict
CC treatment response. The present sequence is human CC chemokine receptor 3
CC (CCR3) gene. This gene is used to illustrate the evaluation of PBMC
CC responses to in Vitro treatment with IFN-beta or GA agents by gene
CC expression profiling technology.
XX
SQ Sequence 5791 BP; 1624 A; 1285 C; 1160 G; 1722 T; 0 U; 0 Other;

Query Match 97.4%; Score 3494.4; DB 14; Length 5791;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 3569; Conservative 0; Mismatches 11; Indels 8; Gaps 6;

QY 1 GGATCCCTACCTTCCCATCAGAGCTAGGGGCGATGAGCGCTCTGCTAAGATGGGA 60
DB |||||
DB 433 GGATCCTACCTTCCCATCAGAGCTAGGGGCGATGAGCGCTCTGCTAAGATGGGA 492
QY 61 CCCCAGGAATGTCTCCCTGTGGGCACTTCTTACCAAGATGGGATGGCCAGTGGGTT 120
DB |||||
DB 493 CCCCAGGAATGTCTCCCTGTGGGCACTTCTTACCAAGATGGGATGGCCAGTGGGTT 552
QY 121 AAGTTGGTGTGAGGCGAGAAAAAAGATCTAGTTTGTACTCTTGAGAGTTCTCGGTTT 180
DB |||||
DB 553 AAGTTGGTGTGAGGCGAGAAAAAAGATCTAGTTTGTACTCTTGAGAGTTCTCGGTTT 612
QY 181 GTTCATGGCATGGGCGAGGAGTCAAGGAGCAGCGCTTGCTCAGTGCCTACCAAGTGA 240
DB |||||
DB 613 GTTCATGGCATGGGCGAGGAGTCAAGGAGCAGCGCTTGCTCAGTGCCTACCAAGTGA 672
QY 241 GAAAAAGTGATAGCTGGGCGAGGCGCGCTGTGAGGCGTGTAGTGAACAGA 300
DB |||||
DB 673 GAAAAAGTGATAGCTGGGCGAGGCGCGCTGTGAGGCGTGTAGTGAACAGA 732
QY 301 GAGGCTCTCCATTCCAGCCCAAGGAAGCTAAGATGAATACCTCATGAGTATATTAGC 360
DB |||||
DB 733 GAGGCTCTCCATTCCAGCCCAAGGAAGCTAAGATGAATACCTCATGAGTATATTAGC 792
QY 361 TACAAACCAACACAGAGGTTCCAGAAAAAGGCTCAGCGTTGGAACCAAGTCACCCCAC 420
DB |||||
DB 793 TACAAACCAACACAGAGGTTCCAGAAAAAGGCTCAGCGTTGGAACCAAGTCACCCCAC 852
QY 421 TCAGCAGACACAGTCAATATAATCAAGCAACAAGAGACAGAGACAGAAACCCCTTCCA 480
DB |||||
DB 853 TCAGCAGACACAGTCAATATAATCAAGCAACAAGAGACAGAGACAGAAACCCCTTCCA 912
QY 481 CTCTGCCCATGTCTCAAGTTGAGTGGCCCTTCTCCAGATCTCTGCCACCATCTTAGA 540
DB |||||

DB 913 CTCTGCCCATGTCTCAAGTTGAGTGGCCCTTCTCCAGATCTCTGCCACCATCTTAGA 972
QY 541 AAGCAACACTGAAGAAGAACTGAAATTATTAAGCTGACAGCATAAAGAGATGATAAA 600
DB |||||
DB 973 AAGCAACACTGAAGAAGAACTGAAATTATTAAGCTGACAGCATAAAGAGATGATAAA 1032
QY 601 ACCTAATAATCATTTGTTCCATGAAATGAATCAAGAGAAAGTTTAAACCACTTTGACTTAAA 660
DB |||||
DB 1033 ACCTAATAATCATTTGTTCCATGAAATGAATCAAGAGAAAGTTTAAACCACTTTGACTTAAA 1092
QY 661 TGTGTGAATCCTTTTCTCTGCTATCCAGCAGATGAGAAAGCTGTGTAACAGAGACCAATA 720
DB |||||
DB 1093 TGTGTGAATCCTTTTCTCTGCTATCCAGCAGATGAGAAAGCTGTGTAACAGAGACCAATA 1152
QY 721 GTTTGAGACTAAAGAATCAATGACATTTCACTGCTGAGTGTGATTTGTGAGTAATTTTA 780
DB |||||
DB 1153 GTTTGAGACTAAAGAATCAATGACATTTCACTGCTGAGTGTGATTTGTGAGTAATTTTA 1212
QY 781 GTTGACCTCAC-TTGTGTAATCTTGACACAGGGGCAATCCAATATCTGACAAAGAGATAT 839
DB |||||
DB 1213 GTTGACCTCACCTTTGTGTAATCTTGACACAGGG--CATCCATATCTGCAC-AGAGATAT 1268
QY 840 GTTAACCAAGTGTAAATGCTGCATGAGAGATTTGGGTGATTTTACTTTGTTTTGTGC 899
DB |||||
DB 1269 GTTAA-CAGTGTAAATGCTGCATGAGAGATTTGGGTGATTTTACTTTGTTTTGTGC 1327
QY 900 TCTTTCTTTCTTATTTGTTCTTACTTATTTACGATTAACCTATCGTTTTCCCAAAATGTAAA 959
DB |||||
DB 1328 TCTTTCTTTCTTATTTGTTCTTACTTATTTACGATTAACCTATCGTTTT-CCAAAATGTAAA 1386
QY 960 AGGCCATTTGAAAGCCTAATTCAAACCTCTTCACTATTTTGTATCTAAGTATTCACCTT 1019
DB |||||
DB 1387 AGGCCATTTGAAAGCCTAATTCAAACCTCTTCACTATTTTGTATCTAAGTATTCACCTT 1446
QY 1020 GATTGAGACTGGGTAGACAGGTGAAAAACATATCAGGTTTAAATTTTAAATTTTAAAT 1079
DB |||||
DB 1447 GATTGAGACTGGGTAGACAGGTGAAAAACATATCAGGTTTAAATTTTAAATTTTAAAT 1506
QY 1080 TATTTATTTATTTATTTATTTTGAAGATGAGTCTGGCTGTGCCAGGCTGAGGTGCA 1139
DB |||||
DB 1507 TATTTATTTATTTATTTATTTTGAAGATGAGTCTGGCTGTGCCAGGCTGAGGTGCA 1566
QY 1140 GCGGCGTGATCAAGTTCATGCAAGCTTCAACCTTCAAGGCTCAAGGATTTCTCCACCT 1199
DB |||||
DB 1567 GCGGCGTGATCAAGTTCATGCAAGCTTCAACCTTCAAGGCTCAAGGATTTCTCCACCT 1626
QY 1200 CAGCCCCCAAGTAGTTGGGACCAACGTAAGCGGCCACCATGCTGCTAATTTCTTAT 1259
DB |||||
DB 1627 CAGCCCCCAAGTAGTTGGGACCAACGTAAGCGGCCACCATGCTGCTAATTTCTTAT 1686
QY 1260 TTTTGTAGAGATAGGATCTCATATATTGTCAGAGCTGTGTAATTCCTGGGCTCAG 1319
DB |||||
DB 1687 TTTTGTAGAGATAGGATCTCATATATTGTCAGAGCTGTGTAATTCCTGGGCTCAG 1746
QY 1320 GTGAGCTCCACCTGGGCTGCCAAAGTAAGTGAGTTACAGGCAAGCAAGGTCCCC 1379
DB |||||
DB 1747 GTGAGCTCCACCTGGGCTGCCAAAGTAAGTGAGTTACAGGCAAGCAAGGTCCCC 1806
QY 1380 TGCCCATATGAGATTTTCTGTCTGTATCCCATGCAAGCTAGTAATCAAGGACTTGGCTGC 1439
DB |||||
DB 1807 TGCCCATATGAGATTTTCTGTCTGTATCCCATGCAAGCTAGTAATCAAGGACTTGGCTGC 1866
QY 1440 TGAATCTGAGGAGCACTGCAATGCTTTCTGAGCTGTGAACCTTCAAGTCAATAG 1499
DB |||||
DB 1867 TGAATCTGAGGAGCACTGCAATGCTTTCTGAGCTGTGAACCTTCAAGTCAATAG 1926
QY 1500 GCAGCCCTGAAACCAACCAAAAGGTTCTATGTTTATCATTCCTGATCATGTTGATTTT 1559
DB |||||
DB 1927 GCAGCCCTGAAACCAACCAAAAGGTTCTATGTTTATCATTCCTGATCATGTTGATTTT 1986
QY 1560 ATAGAAATTAACATGATTAAGCACTAACCTCAAACTGAGCAAAACTTAAGTAATTTT 1619
DB |||||
DB 1987 ATAGAAATTAACATGATTAAGCACTAACCTCAAACTGAGCAAAACTTAAGTAATTTT 2046

QY 1620 TTTTAAAGTTTGACCTGTTTTTAAATCACTCTTGAGAAAAAGAAAAATAATACAAATA 1679
 |||||
 Db 2047 TTTTAAAGTTTGACCTGTTTTTAAATCACTCTTGAGAAAAAGAAAAATAATACAAATA 2106
 |||||
 QY 1680 ATTAAAGGTGAATACAGAGCTACTATACCTTTGTTCTCCAGAAATTAGCAGTTCTGTTCTT 1739
 |||||
 Db 2107 ATTAAAGGTGAATACAGAGCTACTATACCTTTGTTCTCCAGAAATTAGCAGTTCTGTTCTT 2166
 |||||
 QY 1740 TCTTGCTTTAGATGCTGAAGTGCAGAAAGCACTGTGATTTGAGTGTGTAAGTACTGACA 1799
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 Db 2167 TCTTGCTTTAGATGCTGAAGTGCAGAAAGCACTGTGATTTGAGTGTGTAAGTACTGACA 2226
 |||||
 QY 1800 AAAATGTATTTTTTTCTCAGCTGCTATGGAATTGATTAATGCTATTAAGTAAGATG 1859
 |||||
 Db 2227 AAAATGTATTTTTTTCTCAGCTGCTATGGAATTGATTAATGCTATTAAGTAAGATG 2286
 |||||
 QY 1860 CTGATGGAGACACACAAACCAATTTGTTCTCAGTCCATTTCCTCCTCAAAAGCCTGG 1919
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 Db 2287 CTGATGGAGACACACAAACCAATTTGTTCTCAGTCCATTTCCTCCTCAAAAGCCTGG 2346
 |||||
 QY 1920 AATGTGCCATTGATCAGTGGAGATGTACCTGACAGACCCCATGAAAAGAGATCAACAAG 1979
 |||||
 Db 2347 AATGTGCCATTGATCAGTGGAGATGTACCTGACAGACCCCATGAAAAGAGATCAACAAG 2406
 |||||
 QY 1980 TTCCACCCCAAGGAGCCCTATTTTCTTAATTTCAATTGGAATGCTTCTAATGTCTTC 2039
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 Db 2407 TTCCACCCCAAGGAGCCCTATTTTCTTAATTTCAATTGGAATGCTTCTAATGTCTTC 2466
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 QY 2040 TTTCAATCTGCTTCTCCTACCAAGTTTACAGCTTTTCTGCTTCAATGTGAATCAAT 2099
 |||||
 Db 2467 TTTCAATCTGCTTCTCCTACCAAGTTTACAGCTTTTCTGCTTCAATGTGAATCAAT 2526
 |||||
 QY 2100 ACACTCTATTTTTCTCTCATCAACAACCCCAAGTGAACCCCAATGTCCTCACTTCGATATA 2159
 |||||
 Db 2527 ACACTCTATTTTTCTCTCATCAACAACCCCAAGTGAACCCCAATGTCCTCACTTCGATATA 2586
 |||||
 QY 2160 AGTAAAGAGGCTCTGCAATTAAGGCTGTTCGAAGGACGCGAGCTGAGAGGCGCTAGAC 2219
 |||||
 Db 2587 AGTAAAGAGGCTCTGCAATTAAGGCTGTTCGAAGGACGCGAGCTGAGAGGCGCTAGAC 2646
 |||||
 QY 2220 TGGCTCATTTTCATCTCTATTTCTCACTGACTTTGACTTACCAAGAACCCCAATGTGG 2279
 |||||
 Db 2647 TGGCTCATTTTCATCTCTATTTCTCACTGACTTTGACTTACCAAGAACCCCAATGTGG 2706
 |||||
 QY 2280 GCGTCAGTATTCGATCAATTAATTTCTAATTAAGAGCAAAACAATCCCGCATTTGCC 2339
 |||||
 Db 2707 GCGTCAGTATTCGATCAATTAATTTCTAATTAAGAGCAAAACAATCCCGCATTTGCC 2766
 |||||
 QY 2340 AGTTATTAAGCATTTCTCAGATTTAATTGAGAAATGCCCATGCCCTGTATATTCAAT 2399
 |||||
 Db 2767 AGTTATTAAGCATTTCTCAGATTTAATTGAGAAATGCCCATGCCCTGTATATTCAAT 2826
 |||||
 QY 2400 CTTCAACCTTTGTCCTTCTCTAGAAAGGAGAAAGTCAAGTTGATGCCCTGTAGAAAC 2459
 |||||
 Db 2827 CTTCAACCTTTGTCCTTCTCTAGAAAGGAGAAAGTCAAGTTGATGCCCTGTAGAAAC 2886
 |||||
 QY 2460 TAGTGATGGCTTAAGTGTCTTTCATGACTCTGCTTATCTGTTTCTATTTCTCTCC 2519
 |||||
 Db 2887 TAGTGATGGCTTAAGTGTCTTTCATGACTCTGCTTATCTGTTTCTATTTCTCTCC 2946
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 QY 2520 TTTTCCACCGAAGTCTATATCTCAAGAAAAGCAGGCACTGGCTTTAGGGCTCTGGCCT 2579
 |||||
 Db 2947 TTTTCCACCGAAGTCTATATCTCAAGAAAAGCAGGCACTGGCTTTAGGGCTCTGGCCT 3006
 |||||
 QY 2580 AAGAAATATCAAGTCCAGTGAAGAAATCCATTGACTGACCCCTCTGCTTACCCTTTGT 2639
 |||||
 Db 3007 AAGAAATATCAAGTCCAGTGAAGAAATCCATTGACTGACCCCTCTGCTTACCCTTTGT 3066
 |||||
 QY 2640 GATGGAAGAGCTCCAGGGGTTGCTTTTGCATGTTACCAAGGCTTAAGTCAAGATCAAC 2699
 |||||
 Db 3067 GATGGAAGAGCTCCAGGGGTTGCTTTTGCATGTTACCAAGGCTTAAGTCAAGATCAAC 3126
 |||||

QY 2700 AGGGGCAAGAAAAGGAAGTAACTTAACTAATGCTGCTTATTAATTGTAATTATTTGTAAT 2759
 |||||
 Db 3127 AGGGGCAAGAAAAGGAAGTAACTTAACTAATGCTGCTTATTAATTGTAATTATTTGTAAT 3186
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 QY 2760 AGTTAATTAATGATTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTG 2819
 |||||
 Db 3187 AGTTAATTAATGATTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTG 3246
 |||||
 QY 2820 TGTGATTTGATTTATGTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 2879
 |||||
 Db 3247 TGTGATTTGATTTATGTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 3306
 |||||
 QY 2880 CTCAAGTCCGTAGCAATTTTCAAAAAGTTAAATTTAAATACTACATTTGATTTGATTTG 2939
 |||||
 Db 3307 CTCAAGTCCGTAGCAATTTTCAAAAAGTTAAATTTAAATACTACATTTGATTTGATTTG 3366
 |||||
 QY 2940 TGAAGAGAAATGACATGATTAAGAGACTAAAGATCTAGCCCAATTTATATTACTT 2999
 |||||
 Db 3367 TGAAGAGAAATGACATGATTAAGAGACTAAAGATCTAGCCCAATTTATATTACTT 3426
 |||||
 QY 3000 GTTAGAGATTTTGAACAAATTAATAATTTCTCAAGTTCAATTTCCCATTAATTAAT 3059
 |||||
 Db 3427 GTTAGAGATTTTGAACAAATTAATAATTTCTCAAGTTCAATTTCCCATTAATTAAT 3486
 |||||
 QY 3060 AATGAATGCTCATCATTAATGAGGCTCTGAGAGAGCATTAATTAATTTGTAATTTGTAAT 3119
 |||||
 Db 3487 AATGAATGCTCATCATTAATGAGGCTCTGAGAGAGCATTAATTTGTAATTTGTAAT 3546
 |||||
 QY 3120 CATTTGTAATTAATTAATTAATTTTCTTTTAAATGATTAAGATTTTAAAGTATAT 3179
 |||||
 Db 3547 CATTTGTAATTAATTAATTAATTTTCTTTTAAATGATTAAGATTTTAAAGTATAT 3606
 |||||
 QY 3180 GTAACTGTAAACATAAATGCAAAATGCGTAAAGAGACATTAATTAATTAATTAATTA 3239
 |||||
 Db 3607 GTAACTGTAAACATAAATGCAAAATGCGTAAAGAGACATTAATTAATTAATTAATTA 3666
 |||||
 QY 3240 TTATATTTGTTATCATTAATTAAGCTGTTTCTCTGTTGTTATTTCTTCTTAAATGTC 3299
 |||||
 Db 3667 TTATATTTGTTATCATTAATTAAGCTGTTTCTCTGTTGTTATTTCTTCTTAAATGTC 3726
 |||||
 QY 3300 TTACAGAAATCTGATCCCAATTTCTTCAACCAACCCCAATTTCTGCTTCTTTCC 3359
 |||||
 Db 3727 TTACAGAAATCTGATCCCAATTTCTTCAACCAACCCCAATTTCTGCTTCTTTCC 3786
 |||||
 QY 3360 CATGCC-EGTCATGCTAATTTGAAAGCTTCAGCTCTTTCTCTCAATCTTCTCTG 3418
 |||||
 Db 3787 CATGCCGGGTCAATGCTAATTTGAAAGCTTCAGCTCTTTCTCTCAATCTTCTCTG 3846
 |||||
 QY 3419 GCACTCTGATATGCTTTGAAATTCATGTTAAAGAAATCCCTAGGCTGCTATCACATGT 3478
 |||||
 Db 3847 GCACTCTGATATGCTTTGAAATTCATGTTAAAGAAATCCCTAGGCTGCTATCACATGT 3906
 |||||
 QY 3479 GGCATCTTTGTTGATGATGATTAATCAACTGTTGTTTAAAGAGATGATTAATGC 3538
 |||||
 Db 3907 GGCATCTTTGTTGATGATGATTAATCAACTGTTGTTTAAAGAGATGATTAATGC 3966
 |||||
 QY 3539 TTCAATTTGGATTTGATTTTCTTCTTCTATCAAGGAGAGATGAA 3586
 |||||
 Db 3967 TTCAATTTGGATTTGATTTTCTTCTTCTATCAAGGAGAGATGAA 4014
 |||||

RESULT 4
 ABL32337/c
 ID ABL32337 standard; DNA; 7201 BP.
 XX ABL32337;
 AC
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DB Human immune system associated gene SEQ ID NO: 310.
 XX Human immune system disease; cytosine methylation; antiasthmatic;
 KW antiarteriosclerotic; antihaemic; cyostatic; nootropic;
 KW

Db 4256 AACCTTAAACCACAAACCAAAATTTCTAATATTATCATCCGATCATATTAATTTAT 4197
Qy 1562 AGAAATAACACATGAATTAAGACATACTCAAACTGAGCAAACTTAAGTAATTTT 1621
Db 4196 AAAAATAACACATAAATTA AAAACATACTCAAACTAAACAAACTTAATTAATTTT 4137
Qy 1622 TTAAGTTTGACCTGTTTTTAATCACTCTTGAGAGAAAAAGAAATAAATACAATAT 1681
Db 4136 TTAATAATTAACTATTTTAAATCACTCTTA AAAAAAATAAATAACAATATAT 4077
Qy 1682 TAACTGTAATACAGGCTACTATACCTTTGTTCTCCAGATTAAGAGTTCTGTTTC 1741
Db 4076 TAAAGTAATAACAACTACTATACCTTTATTTCTCAAAATTAACAATTTCTTTC 4017
Qy 1742 TTGCTTTAGATGCTGAAGTGCAGAGACACTCTGTGATTTGACGTGTACTGACAAA 1801
Db 4016 TTACTTTAAATACTAAATAACAAAAACA CTATATATTAAGTATATACTAACAAA 3957
Qy 1802 ATGTGATTTTTTTTCTCAGCTGCTATGAGATTGATTATGCTATTAAGTAAGATGCT 1861
Db 3956 ATATATATTTTTTTCTCAACTACTATAAATTAATTAATTAATTAATAAATACT 3897
Qy 1862 GATGGAGCACACACAACCAATTTGTTCTCAGTCCATTTTCTCTCAAAAGCTGAA 1921
Db 3896 AATTAACACACACACAACCAATTTATTTCTCAATCCATTTCTCTCAAAACCTAAA 3837
Qy 1922 TGTGCCATTTGATCAGTGGAGATGACCTGACAGACCCATGAAGAGATCAACAAT 1981
Db 3836 TATACATTTAATCAATTAATAAATATACCTAAACAACCCATTAATAAATAATCAACAAT 3777
Qy 1982 CCACCAAGGACCCCTATTTTCTTAATTTCAATTTGAATGCTTTCAATTTGCTCTT 2041
Db 3776 CCACCAAAAAACCCCTATTTTCTTAATTTCAATTTGAATGCTTTCAATTTGCTCTT 3717
Qy 2042 TCATTCCTGCTTCTACCAAGTTTACAGCTTTTCTGTTTCAATGTGAATCTACATAC 2101
Db 3716 TCATTCCTACTTCTCAACCAATTTTACACTTTTCTAATTTCAATATAAATCTACATAC 3657
Qy 2102 ACTTCATTTTTTCTCATCAACAACCCCAAGTGAACCAATGTCCTCACTTTCATATAAG 2161
Db 3656 ACTTCATTTTTTCTCATCAACAACCCCAATAAATTAATTCCTCACTTTCATATAA 3597
Qy 2162 TAAAGAGGCTCTGCATTAAGGCTTTGTCGAAGGCAAGCAGCTGAGAGGCGCTAGGACTG 2221
Db 3596 TAAAAAAAATCTCATTAATAAACTTATTCAAAAACAGCAACTAATAAAACGCTAAACTTA 3537
Qy 2222 GCTCCATTTTCCATCTCTATTTCTCACTGACTTTGACTTACCCAGAACCCCAATGTGGGC 2281
Db 3536 ACTCCATTTTCCATCTCTATTTCTCACTTAACCTTAACCCAAACCCCAATATAAAG 3477
Qy 2282 CTCAGTATTCGATCAATTAATTCATTAAGAAGCAAAAAACAATCCCGCATTTGCCCCAG 2341
Db 3476 CTCATATTCGATCAATTAATTCATTAATAAAACAATAAACAATTCGCCGATTAACCCCAA 3417
Qy 2342 TTAATAAGCATTTTCTCAGATTACCTTGAAGAAATGCCCATGCGCTGTATATTCAATCT 2401
Db 3416 TTAATAACATTTCTCAATTTTACCTTAATAAATACCCCATGACCTATATAATTCAATCT 3357
Qy 2402 TCACCTTGTCTCTCTCTCTAGAAAGAGAAAGTCAAGTTGATGCGCTCTGAGAACTA 2461
Db 3356 TCACCTTATCCCTTCTCTCAAAAAAATAAATAAACAATTAATAACCTCAAAAAACTA 3297
Qy 2462 GTGCAAGGCTTAAGTGTCTCTCATGACTCTGCGCTATCTGTTTCTATTTTCTCTCT 2521
Db 3296 ATACATACTTAATCTATCTCTCAATACTCTTACCTTATCTATTTTCTATTTTCTCTCT 3237
Qy 2522 TTCACCGAAGTCTATATCTCAAGAAAGCAGGCACTGCGCTTAGGGCTCTCGCCTAA 2581
Db 3236 TTCACCGAAGTCTATATCTCAAAAAAACAACAACATACTTAATAACTCTTAACCTAA 3177
Qy 2582 GAAATATCAAGTCCAGTGAGAAATCCGATTTGACTGACCCCTCTGCTTACCCCTTTGTA 2641

Db 3176 AAAATATCAAAATCCAAATAAAAAATCCCATTAACTAACCCCTCTACTTACCCCTTATAA 3117
Qy 2642 TGGAGAGCTCCAGGGGTTTGTCTTTTGGATGTTACAGGCTTAACCTCAGCATCACCAG 2701
Db 3116 TAAAAAAATCCCAAAAAATTACTTTTAGATATTAACCAAACTTAACCTCAACATCACCA 3057
Qy 2702 GGGCAAGAAAAAGAAAGTAACCTAACTAATGCTGCTTATTAATTGTAATTATGTAATAG 2761
Db 3056 AAACAAAAAATAAATAAATACTTAATACTAATTAATTAATTAATTAATTAATAA 2997
Qy 2762 TTAATTACTGTGATTTGTACATGTGTAAACAGACAAAATGTGTATTTTTTTCACAGCTGTG 2821
Db 2996 TTAATTACTATTAATTAATTAATTAATAAACAACAATAATATATTTTTTTCACACTACTA 2937
Qy 2822 TGGATTGATTATGCCATTTTGAATTAAGAAATGCTGTTAAGAGACACAAGCCAGTTCT 2881
Db 2936 TAAATTAATTAATTAACATTTAAATAAATACTATTAATAACACACAACCAATTCCT 2877
Qy 2882 CAAGTCCGTAGCAAAATTTTCAAAAGTTAAATTTAAAAATCACTAATTTGAATCTAGTG 2941
Db 2876 CAATCCGTAAACAATTTTCAAAAATTAATTTAAAAATCACTAATTTAAATCTAATA 2817
Qy 2942 ACAGAGAAATGGAATGGAATGAGACTAAGATCTAGCCCAATTTTATATTACTTGT 3001
Db 2816 ACAAAAAATAAACAATAATTAATAAATACTAACCCTAATTTATATTACTTAT 2757
Qy 3002 TAGAGATTTTGAACAATTACTAATTTGTTCAAGTTCAATTTCCCATTAACCTATAA 3061
Db 2756 TAAATAATTTTAAACAATTACTAATTTCTCAAAATTCATTTCCCATTAACCTATAA 2697
Qy 3062 TGAATGCTCATCATTAATGAGGCGCTGAGAGAGCATTAATTAATTTGAATTAATTAATCA 3121
Db 2696 TAAATACTCATCATTAATAAACCTTAATAAACAATAATTAATTAATTAATTAATTAATCA 2637
Qy 3122 TTGTTAATTAATTAATTAATTAATTTGCTTTTAATGGAATGGAATTTTAAGTATATGT 3181
Db 2636 TTAATTAATTAATTAATTAATTAATTTTAAATTAATTAATTAATTAATTAATTAAT 2577
Qy 3182 AAACGTAAAAATTAATAATGCAAAATGCCCTTAAGAGACAGTAATTAATTAATTAAT 3241
Db 2576 AAACGTAAAAATTAATAATGCAAAATGCCCTTAATAAATAAATAATTAATTAATTAAT 2517
Qy 3242 AATATGTTATCATTAATTAAGCTGTTTTTCTCTGTTGTAATTTCTCTTAATAGCTT 3301
Db 2516 ATATTAATTAATCATTAATTAACCTAATTTTCTCTATTTTAATTTCTCTTAATACTT 2457
Qy 3302 ACAGAAATCTGTATCCCATTTCTCAACCAACAACCCCAACAATTTCTGCTCTTTCCCA 3361
Db 2456 TCAAAAATCTATATCCCATTTCTCAACCAACAACCCCAACAATTTCTGCTCTTTCCCA 2397
Qy 3362 TGCCG-GTCATGCTAATTTGAAGCTTCAGCTCTTCTCTCAATCTCTCTGCG 3420
Db 2396 TACCGAATCATTAATTAATTAATAAATTAATAAATTAATAAATTAATAAATTAATAA 2337
Qy 3421 ACCCTGATATGCTTTTGAATTCATGTTAAAGAAATCCCTAGGCTGCTATCAATGTGG 3480
Db 2336 ACCCTAATATACCTTTTAAATTCATTAATTAATAAATTAATAAATTAATAAATTAATAA 2277
Qy 3481 CATCTTGTGAGTACATGAATAAATCAACTGTGTGTTTGAAGAGATGATTAATGCTT 3540
Db 2276 CATCTTAATTAATACATAAATAAATCAACTAATATATTTTGAAGAAATAATTAATACTT 2217
Qy 3541 CATGTGGAGTGTATTTTCTCTCTTCTATCAAGGAGAGATGA 3586
Db 2216 CATTAATAAATTAATTTTCTCTCTATCACAAAAAAATAA 2171

RESULT 5
ABL32336
ID ABL32336 standard, DNA; 7201 BP.
XX
AC ABL32336;
XX

QY	1441	GACTCTGAGGACCTGCAGCTTCTTGAGCTGTGAACCTGCAGTGTAAAGCTCATAGG	1500
Db	2885	GATTTTGAGGATTTGTAAGTTTTTTGAGTGTGAATTTTAAGTTAAAGTTTAAGG	2944
QY	1501	CAGCCGTGAACCCAAACCAAGGTTCTATGTTTATCATCTGTATCATGTGTGATTTTA	1560
Db	2945	TAGTTTGAATTTAAATTAAAGGTTTATGTTTATTAATTTCGATTATGTGATTTTA	3004
QY	1561	TAGAATAACACATGAATTAAAGACACTACCTCAACCTGAGCAAACTTAAGTAATTTT	1620
Db	3005	TAGAATAATATATGAATTAAAGATATTAATTTTAAATTGAGTAATAATTTAAGTAATTTT	3064
QY	1621	TTTAAAGTTTGACCTGTGTTTTAAATCACTCTTGAGAAAAGGAAATTAATACAAATAA	1680
Db	3065	TTTAAAGTTTGATTGTTTTTAAATTAATTTTGGAGAAAAGGAAATTAATTAATAATAA	3124
QY	1681	TTAACGGTGAATACAGGCTACTATACCCTTGTTCTCCAGAAATTAAGCAGTTCTGTTCTTTT	1740
Db	3125	TTAACGGTGAATATAGGCTATATATATTTTGTGTTTAAAGAAATTAAGTATTTGTTTCTT	3184
QY	1741	CTTGCTTAGATGCTGAAGTGCAGAAGGACACTCTGTGAATTGTACGTGTAACTGACAA	1800
Db	3185	TTTGCTTTAGATGTGAAGTGTAGAAGGATATTTGTGATTTGTACGTGTGTAATTGATAA	3244
QY	1801	AATGTGATTTTTTTTCTCAGCTGCTATGGAATTGGAATATGCTATTATGAATAAGAAATGC	1860
Db	3245	AATGTGATTTTTTTTTTAACTGTATGGAATTGGAATATGCTATTATGAATAAGAAATGT	3304
QY	1861	TGATGGAGCACACAAACCATTTGTTCTCAGTCCATTTTCTCTCCAAAGCCTGGA	1920
Db	3305	TGATGGAGTATATATAAATTAATTTGTTTTTAACTTAATTTTAAAGTTTGA	3364
QY	1921	ATGTGCCATTGATCAGTGGAGATGTACTGGAAGAACCATGAAAAGATCAACAAGT	1980
Db	3365	ATGTGTTATTTGATAGTGGAGATGATTTTGATAGATTAATGAAGAAAGATTAATAAGT	3424
QY	1981	TCCACCCCAAGGACCCATTTTTCTTAATTTCAATTTGAAATGCGCTTCTAATTTGCTCTT	2040
Db	3425	TTTATTTAAGGATTTTATTTTTTTTAAATTTTGAATGCTTTTAAATTTGTTTTTTT	3484
QY	2041	TTCATTCCTGCTTCTTACCAAGTTTACAGCTTTTCTGTGTTCAATGTGAATCTACATA	2100
Db	3485	TTTATTTTGTGTTTTTATTAAGTTTATAGTTTTTTTGTGTTTAAATGTGAATTTATATA	3544
QY	2101	CACCTCTATTTTTCTCTATCAACAACCCCAAGTGACCCAAATGCTCTCACTTGCATATAA	2160
Db	3545	TATTTTATTTTTTTTTTATATAATTTAAGTATTAATGTTTTTATTTTGCATATAA	3604
QY	2161	GTAAGAAGGCTCTGCATTAAGGGCTGTGCCAAGGCAAGCACTGAGAGCGCTAGACT	2220
Db	3605	GTAAGAAGGTTTGTATTAAGGGTGTGTTAAGGTAAGTATGAGAGCGCTTAGACTT	3664
QY	2221	GGCTCCATTTCCATCTCTATTTCTCACTGACTTTGACTTACCAAGAACCCCAACATGTGGGG	2280
Db	3665	GCTTTTATTTTATTTTATTTTATTTTGAATTTGATTTATTAAGAAATTTTAAATATATGIGGG	3724
QY	2281	CCTCAGTATTCGATCAATTAATCTATTAAGAGCAAAAACAATCCCGCATTTGGCCCCA	2340
Db	3725	TTTATGATTCGATTAATTAATTTTATTAAGAAAGTAAATAATTTTTCGTATGTGTTTA	3784
QY	2341	GTTATTAAGCATTTCTCAGATTACCTTGAGAAATGCCCATCGGCTGTATATTCAATC	2400
Db	3785	GTTATTAAGTATTTTATTAAGTTATTTTGAGAAATGTTTATCGGTTGTATATTATATAT	3844
QY	2401	TTCAACCTTGTCCCTTCTCTAGAAAGAGAAAGTCAATTGGAATGCCCTTGAGGAAT	2460
Db	3845	TTTATTTTGTGTTTTTTTTTTTGAAGAAAGAAAGTATGATGTTTTTTTGAGAGAAAT	3904
QY	2461	AGTGCATGGCTTAACGTGTCTTCCAATGACTCCTGCCTTATCTGTTTCTATTTTCTCTCT	2520
Db	3905	AGTGTATGCTTTAATTTGTTTTTTTATGATTTTGTGTTTATTTGTTTTTATTTT	3964

QY	2521	TTTCCACC	GAGTCTA	TAAATCT	CAAGAA	AGCAG	GGCACT	GGCCTT	AGGGCT	CTCG	GCCTA	2580
Db	3965	TTTTTAT	CGAAGTT	TAATAAT	TTTAAGA	AAAGTA	GGTAAT	TGGTTT	TAAGGG	TTTTGG	TTTTA	4024
QY	2581	AGAAAT	ATCAAGT	CCAGTGA	AAATCC	CATGAC	TGACCC	CTCGCT	TACCC	TTTG	2640	
Db	4025	AGAAAT	ATTAA	GTTAGT	GAGAA	ATTAT	TGAAT	TGATTT	TTTGT	TTATTT	TTTGTG	4084
QY	2641	ATGAGA	AGCTCC	AGGGTT	GTCTTT	TGACGT	TACAG	GCCTA	AGC	TACCA	2700	
Db	4085	ATGAGA	AGCTTT	TAGGG	TTGT	TTTGTAT	GTATAG	GTTAAT	TATAG	TATATTA	4144	
QY	2701	GGGGCA	AGAAAG	AAAGTA	ACCTAA	CTAAT	GTCTTA	TATTT	GTATTA	TTGTATA	2760	
Db	4145	GGGGTA	AGAAAG	AAAGTA	ATTAA	TTAAT	TATGT	TTTAT	TATGT	TATTA	4204	
QY	2761	GTTAAT	TACTGT	ATGTTGA	CATGTGT	ACAGACA	CAAAAT	GTGTAT	TTTTT	GCAGCT	2820	
Db	4205	GTTAAT	TATGT	ATGTTGA	TATGTGT	ATAGATA	AAATGT	GTATTT	TTTAT	AGTTGT	4264	
QY	2821	GTGAT	TGATTAT	GCCATT	TGGAAT	AAGTCT	GTAA	GACAC	ACAAG	CCAGT	2880	
Db	4265	GTGAT	TGATTAT	GTATTT	TGGAATA	GAATGT	GTAA	GATAT	ATAGT	TAGT	4324	
QY	2881	TCAAGT	CCGTAG	CAATTT	TTCAAA	AGTTAA	ATTAAAA	TCACT	ACATTT	GAATCT	2940	
Db	4325	TTAAGT	CTGTAG	TAAATTT	TTTAAAG	TTAAAT	TTTAAAT	TATAT	TATTT	GAATTA	4384	
QY	2941	GACAGA	GAATGA	CATGGA	TAGAG	CTAA	AGCTTA	GCCCAA	TTTAT	TATTA	3000	
Db	4385	GATAGA	GAATGA	TATGAT	AGATGA	GATTAA	GAATTA	GTAA	TTTAT	TATTA	4444	
QY	3001	TTAGAG	ATTTTGA	CAAA	TCTAA	ATTTCT	TCAAG	STCA	ATTTCC	CCATTA	3060	
Db	4445	TTAGAG	ATTTTGA	TAAAT	TATTA	ATTTTT	TAAAG	STTA	ATTTTT	TAAATTA	4504	
QY	3061	ATGAAT	GTCTCA	TATAT	TGGGGC	CTGAGA	GCATAT	TACT	GTAA	TGTAA	3120	
Db	4505	ATGAAT	GTCTTAT	TATAT	TGGGGT	TTTGAGA	GCATAT	ATAT	TATTT	GTATGT	4564	
QY	3121	ATTGTT	ATTATT	ATATAC	ATTTT	TGCTTT	TAAAT	TGAT	TAAG	ATATG	3180	
Db	4565	ATTGTT	ATTATT	ATATAT	ATTTT	TGCTTT	TAAAT	TGAT	TAAG	ATATG	4624	
QY	3181	TAAACT	GTAAAA	CAATAA	ATGC	AAATGCC	TAA	GAGACA	GTAGT	ATAATA	3240	
Db	4625	TAAAT	GTAAAA	CAATAA	ATGTG	TAA	GAGACA	GTAGT	ATAATA	ATATAT	4684	
QY	3241	TATAT	TGTAT	ATCTA	TCTAG	CTGT	TTTCC	TGTGT	ATTTCT	CTTAA	3300	
Db	4685	TATAT	TGTAT	ATCTA	TCTAG	CTGT	TTTCC	TGTGT	ATTTCT	CTTAA	4744	
QY	3301	TACAGA	AAATCT	GTATCC	CAATCT	TAC	ACCAC	CAATTT	CTGCT	TTCC	3360	
Db	4745	TTTGA	AAATCT	GTATTT	TATTT	TATTT	TATTT	TATTT	TATTT	TATTT	4804	
QY	3361	ATG-CC	GTCA	GTAA	CTTG	AAAG	CTTG	AGCT	CTTCC	TCTCA	3419	
Db	4805	ATGTC	GGGTAT	GTAA	TTTGA	AAAGTT	TAGTT	TTT	TTT	TTT	4864	
QY	3420	CACCT	CTGAT	ATGCC	TTTGA	AATTCAT	GTAA	GAATCC	TAGG	CTAT	3479	
Db	4865	TATTT	TGAT	ATGTTT	TGA	AATTTAG	TAA	GAATTT	TAG	GTAT	4924	
QY	3480	GCAT	CTTTG	TGAT	ACAT	GAATA	ATCA	CTG	GTGT	TTTAC	3539	
Db	4925	GTA	TTTTT	TGTA	TATGA	ATAATTA	ATG	GTGT	TTTAC	GAAGAT	4984	
QY	3540	TCA	TTGT	GGAT	GTATTT	TTCTT	CTAT	CA	GGGA	AGTGA	3586	
Db	4985	TTA	TTGT	GGAT	GTATTT	TTCTT	CTAT	CA	GGGA	AGTGA	5031	

ID	Accession	Standard	CDNA	Length (BP)
RESULT 6	AAT85162	standard	CDNA	1915 BP.
AC	AAT85162;			
DT	14-DEC-1997	(first entry)		
DE	Human chemokine receptor 88-2B	cdna.		
XX				
KW	Chemokine receptor 88-2B; atherosclerosis; rheumatoid arthritis; tumour;			
KW	asthma; viral infection; AIDS; inflammation; autoimmune disease; therapy;			
KW	diagnosis; leukocyte trafficking; G protein coupled receptor; human; ss.			
XX				
OS	Homo sapiens.			
FH	Key	Location/Qualifiers		
FT	CDS	362..1429		
FT		/*tag= a		
XX				
PN	W09722698-A2.			
XX				
PD	26-JUN-1997.			
XX				
PF	20-DEC-1996;	96WO-US020759.		
XX				
PR	20-DEC-1995;	95US-00575967.		
PR	07-JUN-1996;	96US-00661393.		
XX				
PA	(ICOS-) ICOS CORP.			
XX				
PI	Gray PW, Schweickart VL, Raport CJ;			
XX				
DR	WPI; 1997-341689/31.			
XX				
DR	P-PSDB; AAW27124.			
XX				
PT	New nucleic acid encoding chemokine receptors 88-2B and 88C - used to			
PT	modulate leukocyte trafficking, e.g. for treatment of inflammation,			
PT	tumours, viral infections, auto-immune diseases, etc.			
XX				
PS	Claim 7; Page 48-50; 65pp; English.			
XX				
CC	This sequence comprises a full-length cDNA coding for novel human			
CC	chemokine receptor 88-2B (AAW27124), a G protein coupled receptor that is			
CC	involved in leukocyte trafficking. The 88-2B cDNA was obtained from a			
CC	macrohage cDNA library using 88-2B-specific primers. A full-length clone			
CC	(see AAT89161) for chemokine receptor 88C (AAW27123) was also obtained.			
CC	88C and 88-2B cDNAs can be used to produce recombinant polypeptides in			
CC	transformed host cells for use in the treatment of e.g. atherosclerosis,			
CC	rheumatoid arthritis, tumours, asthma, viral infection, AIDS and			
CC	inflammatory conditions. Nucleic acid fragments can be used to isolate			
CC	genomic sequences, to detect alleles of the gene (for diagnosis or in			
CC	gene therapy), to alter receptor genetics to facilitate identification of			
CC	modulators and to produce knockout animals, and (antisense forms) to			
CC	alter/study the genetics and expression of the receptor			
XX				
SQ	Sequence 1915 BP; 488 A; 470 C; 373 G; 584 T; 0 U; 0 Other;			
XX				
QY	Query Match	9.6%;	Score 344.2;	DB 2; Length 1915;
Db	Best Local Similarity	98.9%;	Pred. No. 1.5e-64;	
Db	Matches 357; Conservative	0;	Mismatches 3;	Indels 1; Gaps 1;
QY	3227	ATAATAATGATTATATATGTTATCATCTATCTAGCCGTGTTTTTTCCTGTGTGTAATTC		3286
Db	1	ATAATAATGATTATATATGTTATCATCTATCTAGCCGTGTTTTTTCCTGTGTGTAATTC		60
QY	3287	TTCCTTTAATGCTTACAGAAATCTGTATCCCATCTTTCACCAACCCCAACAATT		3346
Db	61	TTCCTTTAATGCTTACAGAAATCTGTATCCCATCTTTCACCAACCCCAACAATT		120
QY	3347	CTGCTTCTTTTCCCATGCC-GGTTCATGCTAATTGAAAGCTTCAGCTCTTCCCTTC		3405
Db	121	CTGCTTCTTTTCCCATGCCGGGTTCATGCTAATTGAAAGCTTCAGCTCTTCCCTTC		180

QY	3406	AATCCTTCTCTGGGCACTCTGATATGCCCTTTGAAATTCATGTGTAAGAAATCCCTAGGC	3465
Db	181	AATCCTTTTCTGGGCACTCTGATATGCCCTTTGAAATTCATGTGTAAGAAATCCCTAGGC	240
QY	3466	TGCTATCACATGTGGCATCTTTGTTGAGTACATGAATAAATCAACTGGTGTGTTTACGA	3525
Db	241	TGCTATCACATGTGGCATCTTTGTTGAGTACATGAATAAATCAACTGGTGTGTTTACGA	300
QY	3526	AGGATGATTATGCTTCATTGTGTGGATTGTAATTTCTCTTCTATCACAGGAGAAAGTGA	3585
Db	301	AGGATGATTATGCTTCATTGTGTGGATTGTAATTTCTCTTCTATCACAGGAGAAAGTGA	360
QY	3586	A 3586	
Db	361	A 361	
RESULT 7			
ID	ADC03342	standard; cDNA; 1915 BP.	
XX	AC	ADC03342;	
XX	DT	18-DEC-2003 (first entry)	
XX	DE	Human cDNA encoding chemokine receptor 88-2B.	
XX	KM	88; gene; human; anti-HIV; virucide; HIV; SIV; 88-C; 88-2B;	
KM	KW	chemokine receptor; envelope protein; atherosclerosis;	
KW	KM	rheumatoid arthritis; tumour growth suppression; asthma; viral infection;	
KW	AIDS;	inflammatory condition; chromosome 3p21.	
OS	Homo sapiens.		
XX	Key	Location/Qualifiers	
FT	CDS	362..1429	
FT		/*tag= a	
FT		/product= "Chemokine receptor 88-C"	
FT		/note= "This CDS, minus the STOP codon, is specifically	
FT		claimed in claim 11"	
XX	PN	US2002150888-A1.	
XX	XX	17-OCT-2002.	
PD	XX	26-MAR-2002; 2002US-00106623.	
XX	PF	20-DEC-1995; 95US-00575967.	
PR	XX	07-JUN-1996; 96US-00661393.	
PR	XX	20-DEC-1996; 96US-00771276.	
XX	PA	(GRAY/) GRAY P W.	
PA	PA	(SCHW/) SCHWEICKART V L.	
PA	PA	(RAPO/) RAPOPORT C J.	
PI	Gray PW,	Schweickart VL, Raport CJ;	
XX	XX	WPI, 2003-182491/18.	
DR	DR	P-PSDB; ADC03343.	
XX	PT	Screening for a modulator of HIV and SIV infection utilizing	
PT	PT	polynucleotides that encode the 88C or 88-2B chemokine receptors, useful	
PT	PT	for diagnosing and treating disorders such as atherosclerosis, arthritis,	
PT	PT	AIDS and asthma.	
XX	PS	Claim 11; Page 18-20; 29pp; English.	
XX	PS	The invention relates to screening for a modulator of human	
CC	CC	immunodeficiency virus (HIV) or simian immunodeficiency virus (SIV)	
CC	CC	infection, comprising contacting a first composition having an human	
CC	CC	(ADC03341) or macaque (ADC03359) 88C chemokine receptor polypeptide with	
CC	CC	a second composition having an HIV or SIV envelope protein in the	

CC presence or absence of a compound. Also included are screening for a
CC modulator of HIV infection, detecting HIV infection of cells (comprising
CC contacting a cell that has been recombinantly modified to express at
CC least one of human chemokine receptors 88C and 88-2B with HIV, and
CC detecting HIV infection in the cell) and inhibiting HIV infection of
CC cells (comprising contacting cells with an antibody to at least one of
CC human chemokine receptors 88C and 88-2B with HIV, and detecting HIV
CC infection of the cell after the contacting step). The methods and
CC compositions of the present invention are useful for the diagnosis and
CC treatment of disorders associated with the aberrant expression or
CC activity of 88C or 88-2B chemokine receptors, such as atherosclerosis,
CC rheumatoid arthritis, tumour growth suppression, asthma, viral infection,
CC AIDS and other inflammatory conditions. The genes for human 88-C and 88-
CC 2B are located on chromosome 3p21. The present sequence encodes human
CC chemokine receptor 88-2B.

XX SQ Sequence 1915 BP; 488 A; 470 C; 373 G; 584 T; 0 U; 0 Other;

Query Match 9.6%; Score 344.2; DB 10; Length 1915;
Best Local Similarity 98.9%; Pred. No. 1.5e-64;
Matches 357; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 3227 ATAAATAAGATTATATATGTTATCATATATCTAGCCGTGTTTCTCGTGTGATATTC 3286
|||||
Db 1 AATAATAAGATTATATATGTTATCATATATCTAGCCGTGTTTCTCGTGTGATATTC 60

QY 3287 TTCCTTAAATGCTTACAGAAATCTGATCCCATCTTACACCAACCCACAAACATTT 3346
|||||
Db 61 TTCCTTAAATGCTTACAGAAATCTGATCCCATCTTACACCAACCCACAAACATTT 120

QY 3347 CTGCTTCTTTTCCCATGCC-GGTACGTCTAATCTTGAAGCTTCAGCTTTCTCCTTC 3405
|||||
Db 121 CTGCTTCTTTTCCCATGCCGGGTACGTCTAATCTTGAAGCTTCAGCTTTCTCCTTC 180

QY 3406 AATCCTTCTCTGGCACCTCTGATATGCTTTGAAATTCATGTTAAAGATCCCTAGGC 3465
|||||
Db 181 AATCCTTCTCTGGCACCTCTGATATGCTTTGAAATTCATGTTAAAGATCCCTAGGC 240

QY 3466 TGCCTATCACATGTCATCTTTGTTGAGTACATGAATAATCACTGCTGTTTACGA 3525
|||||
Db 241 TGCCTATCACATGTCATCTTTGTTGAGTACATGAATAATCACTGCTGTTTACGA 300

QY 3526 AGGATGATATGCTTCAATGTTGGAATTTCTTCTTATCACAGGAGAAAGTGA 3585
|||||
Db 301 AGGATGATATGCTTCAATGTTGGAATTTCTTCTTATCACAGGAGAAAGTGA 360

QY 3586 A 3586
|
Db 361 A 361

RESULT 8
ADT90848
ID ADT90848 standard; cDNA; 1915 BP.

XX AC ADT90848;
XX DT 16-DEC-2004 (first entry)

DE Human chemokine receptor 88-2B cDNA.

KW Chemokine receptor 88C; chemokine receptor 88-2B;
KW human immunodeficiency virus; simian immunodeficiency virus; HIV; SIV;
KW infection; vaccine; virucide; gene; ss.

OS Homo sapiens.
XX Key

FT 5'UTR 1..361 Location/Qualifiers
FT CDS /*tag= a
FT CDS 362..1429 /*tag= C
FT /*product= "Human chemokine receptor 88-2B protein"

FT misc_feature 362..469
FT /*tag= b
FT /note= "Encodes extracellular domain"
FT misc_feature 539..574
FT /*tag= d
FT /note= "Encodes extracellular domain"
FT misc_feature 638..682
FT /*tag= e
FT /note= "Encodes intracellular domain"
FT misc_feature 752..814
FT /*tag= f
FT /note= "Encodes intracellular domain"
FT misc_feature 872..949
FT /*tag= g
FT /note= "Encodes extracellular domain"
FT misc_feature 1016..1081
FT /*tag= h
FT /note= "Encodes extracellular domain"
FT misc_feature 1148..1213
FT /*tag= i
FT /note= "Encodes intracellular domain"
FT misc_feature 1277..1426
FT /*tag= j
FT /note= "Encodes intracellular domain"
FT 3'UTR 1430..1915
FT /*tag= k

XX PN US6797811-B1.

XX PD 28-SBP-2004.

XX PF 20-DEC-1996; 96US-00771276.

XX PR 20-DEC-1995; 95US-00575967.

XX PR 07-JUN-1996; 96US-00661393.

XX PA (ICOS-) ICOS CORP.

XX PI Gray PW, Schweickart VL, Raport CJ;

XX DR WPI; 2004-687775/67.

XX DR P-PSDB; ADT90849.

XX PT New antibodies specifically binding to (the extracellular domain of) a
PT chemokine receptor 88C polypeptide expressed on the surface of cells,
PT useful for inhibiting human or simian human immunodeficiency infection of
PT such cells.

XX PS Example 2; SEQ ID NO 3; 29pp; English.

XX CC The invention relates to a novel antibody that specifically binds to the
CC extracellular domain of a chemokine receptor 88C or 88-2B polypeptide
CC expressed on the surface of cells. The antibody fails to cross-react with
CC an MCP-1 receptor (CCR-2) and is useful for inhibiting human or simian
CC immunodeficiency virus (HIV or SIV) infection of the cells expressing
CC chemokine receptor 88C or 88-2B. The invention is also used to detect 88C
CC or 88-2B gene products their analogues or biologically active fragments.
CC The antibody products may be used to as modulators of receptor activities
CC or to diagnose tissue-specific variations in expression of 88-2B or 88C.
CC The invention is also used in the preparation of vaccines. The present
CC sequence is the human chemokine receptor 88-2B cDNA.

XX SQ Sequence 1915 BP; 488 A; 470 C; 373 G; 584 T; 0 U; 0 Other;

Query Match 9.6%; Score 344.2; DB 13; Length 1915;
Best Local Similarity 98.9%; Pred. No. 1.5e-64;
Matches 357; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 3227 ATAAATAAGATTATATATGTTATCATATATCTAGCCGTGTTTCTCGTGTGATATTC 3286
|||||
Db 1 AATAATAAGATTATATATGTTATCATATATCTAGCCGTGTTTCTCGTGTGATATTC 60

QY 3287 TTCCTTAAATGCTTACAGAAATCTGATCCCATCTTTCACCAACCCACAAACATTT 3346

Db 61 TTCTTTAAATGCTTCAGAAATCTGTATCCCCATCTTCACCAACCCCAACAATTT 120
QY 3347 CTGCTTCTTTTCCCATGCC-GGTCACTACTTGAAGCTTCAGCTCTTCCCTCTC 3405
Db 121 CTGCTTCTTTTCCCATGCCGGGTCTAGTACTTGAAGCTTCAGCTCTTCCCTCTC 180
QY 3406 AATCCTTCTCCTGGCACTCTGTATATGCCCTTTTGAATTCATGTAAAGATCCCTAGGC 3465
Db 181 AATCCTTTTCTGGCACTCTGTATATGCCCTTTTGAATTCATGTAAAGATCCCTAGGC 240
QY 3466 TCGTATCACATGTGGCATCTTTGTTGAGTACATGAATAATCAACTGGTGTGTTTACGA 3525
Db 241 TCGTATCACATGTGGCATCTTTGTTGAGTACATGAATAATCAACTGGTGTGTTTACGA 300
QY 3526 AGGATGATTATGCTTCATTGTGGGATGTATTTTCTTCTTATCACAGGAGAAGTGA 3585
Db 301 AGGATGATTATGCTTCATTGTGGGATGTATTTTCTTCTTATCACAGGAGAAGTGA 360
QY 3586 A 3586
Db 361 A 361

RESULT 9
ADU47727
ID ADU47727 standard; cDNA; 1915 BP.
XX AC ADU47727;
XX DT 10-FEB-2005 (first entry)
XX DE Human chemokine receptor 88-2B cDNA.
XX KW Chemokine receptor; 88C; human immunodeficiency virus;
KW simian immunodeficiency virus; HIV; SIV; MCP-1; CCKR-2; 88-2B;
KW leukocyte trafficking; acquired immune deficiency syndrome; AIDS;
KW psoriasis; rheumatoid arthritis; atherosclerosis; tumour; asthma;
KW viral infection; inflammation; anti-HIV; virucide; antipsoriatic;
KW antiarthritic; antiarteriosclerotic; antiinflammatory; human; gene; ss.
XX OS Homo sapiens.
XX FH Key location/Qualifiers
FT 5'UTR 1..361
FT CDS /*tag= a
FT 362..1429
FT /*tag= b
FT /product= "Chemokine receptor 88-2B "
FT 1430..1915
FT /*tag= c
XX PN US2004230037-A1.
XX PD 18-NOV-2004.
XX PF 04-FEB-2004; 2004US-00772037.
XX PR 20-DEC-1995; 95US-00575967.
PR 07-JUN-1996; 96US-00661393.
PR 20-DEC-1996; 96US-00771276.
XX PA (ICOS-) ICOS CORP.
XX PI Gray PW, Schweickart VL, Raport CJ;
XX DR WPI; 2004-813308/80.
DR P-PSDB; ADU47728.
XX PT Modulating chemokine receptor 88C-mediated human or simian
PT immunodeficiency virus infection comprises administering an antibody that
PT binds to chemokines or a polypeptide comprising an antigen-binding
PT fragment of the antibody.

XX PS Example 2; SEQ ID NO 3; 28pp; English.
XX CC The invention relates to a method of modulating chemokine receptor 88C-
CC mediated human or simian immunodeficiency virus (HIV or SIV) infection of
CC cells. The method comprises administering to a mammalian subject a
CC composition comprising an antibody or a polypeptide comprising an antigen
CC -binding fragment of the antibody, where the mammalian subject is
CC infected with HIV or SIV, and where the antibody is administered in an
CC amount that modulates HIV or SIV infection of 88C-expressing cells in the
CC subject. The antibody is a humanised antibody which specifically binds to
CC the extracellular domain of the chemokine receptor 88C polypeptide and
CC fails to cross-react with an MCP-1 receptor (CCKR-2) or binds to the N-
CC terminal 20 amino acid peptide of the 88C receptor. The invention also
CC provides purified and isolated nucleic acids encoding chemokine
CC receptors, namely 88-2B and 88-C, involved in leukocyte trafficking. The
CC modulators of the chemokine receptors of the invention are useful for
CC treating diseases such as HIV or SIV infection (e.g. acquired immune
CC deficiency syndrome (AIDS)), psoriasis, rheumatoid arthritis,
CC atherosclerosis, tumour growth suppression, asthma, viral infection, or
CC inflammation. The present sequence is the human chemokine receptor 88-2B
CC cDNA.
XX SQ Sequence 1915 BP; 488 A; 470 C; 373 G; 584 T; 0 U; 0 Other;

Query Match 9.6%; Score 344.2; DB 13; Length 1915;
Best Local Similarity 98.9%; Pred. No. 1.5e-64;
Matches 357; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 3227 ATAATAATGATTATATATGTTATCATATATAGCTGTTTTTCCGTGTGATTTTC 3286
Db 1 ATAATAATGATTATATATGTTATCATATATAGCTGTTTTTCCGTGTGATTTTC 60
QY 3287 TTCCTTTAAATGCTTACAGAAATCTGTATCCCATTTCTTCAACCAACCCACAATTT 3346
Db 61 TTCCTTTAAATGCTTACAGAAATCTGTATCCCATTTCTTCAACCAACCCACAATTT 120
QY 3347 CTGCTTCTTTTCCCATGCC-GGTCACTGTAATTGAAAGCTTCAGCTCTTCCCTC 3405
Db 121 CTGCTTCTTTTCCCATGCCGGGTCACTGTAATTGAAAGCTTCAGCTCTTCCCTC 180
QY 3406 AATCCTTCTCCTGGCACTCTGATATGCCCTTTTGAATTCATGTTAAAGATCCCTAGGC 3465
Db 181 AATCCTTTTCTGGCACTCTGATATGCCCTTTTGAATTCATGTTAAAGATCCCTAGGC 240
QY 3466 TCGTATCACATGTGGCATCTTGTGAGTACATGAATAATCAACTGGTGTGTTTACGA 3525
Db 241 TCGTATCACATGTGGCATCTTGTGAGTACATGAATAATCAACTGGTGTGTTTACGA 300
QY 3526 AGGATGATTATGCTTCATTGTGGGATGTATTTTCTTCTTATCACAGGAGAAGTGA 3585
Db 301 AGGATGATTATGCTTCATTGTGGGATGTATTTTCTTCTTATCACAGGAGAAGTGA 360
QY 3586 A 3586
Db 361 A 361

RESULT 10
ACN44478
ID ACN44478 standard; DNA; 54701 BP.
XX AC ACN44478;
XX AC ACN44478;
XX DT 18-NOV-2004 (first entry)
XX DE Human genomic sequence hCG24071.
XX KW Cytostatic; carcinoma; lymphoma; cancer; human; gene; ss.
XX OS Homo sapiens.
XX PN WO2003073826-A2.

QY	1049	ATATCAGGTTTAAATTTTAAATTTTAAATTAATTAATTAATTAATTAATTTTGGAGAT	1108
Db	57991	ACATTGGTTTCCAAATTTTAAAAATGACATCTCTTTTTTTTTTTTTTTTTTTGGAGAC	57932
QY	1109	GGAGTCGTGGCTGTGCCCCAGGCTGGAGTGCAGCGCGGTGATCACAGTTCACTGCAGCCTC	1168
Db	57931	AGTCTGTTCTGTGTGCCAGGCTGGAGTGCAGTGGCACAATCACAGCTCACTGCAGCCTC	57872
QY	1169	AACCTTTAGGCTCAAGGGATTCTCCCACTCAGCCCCCAAGTAAGTTGGGACCACACGT	1228
Db	57871	AACCTCCAGGCTCAGGGGATCCTCCCATCTCAGCCTCCAGTAAGTGGGACCACAGAC	57812
QY	1229	ATGCGCACCAAGCCTGGCTAATTTCTAATTTTTTTGTAGAGATGAGATCTCACTATATT	1288
Db	57811	ACCACCCACCACTACTCTACTAATTTTAAATTTTCTGTAGAGATGGGGTCTCACTATGTT	57752
QY	1289	GTCAGGCTGTCTTGAATTCCTGGGCTCAGGTGAGCCTCCCACTGGGCTCCCAAAGT	1348
Db	57751	GCCCAAGTGTGTTCTTGAACCTCTGGGCTCAAGCAATCTCCCACTCAGCCTCCCAAAGT	57692
QY	1349	ACTGGATTACAGGCATGAGCCAAAGGTCCCCCTGCCCATATGAGATTTTCTGTC	1401
Db	57691	GCTGGACTACAGGCTGTGAGCTACCAACACCAAGTTCAATGTTTGTTTTTTAGAC	57639

CC	ADL08116		
XX	AC	ADL08116;	
XX	DT	20-MAY-2004	(first entry)
XX	DE	Human gene associated with low HDL-C	FABP-3.
KW	KW	Human; ds; SNP; single nucleotide polymorphism;	
KW	KW	high density lipoprotein-C; HDL-C; vascular disease;	metabolic disease;
OS	OS	coronary artery disease; gene.	
XX	XX	Homo sapiens.	
FT	FT	Key	Location/Qualifiers
FT	FT	variation	replace(120178,C)
PN	PN	/tag= a	/standard_name= "Single nucleotide polymorphism"
PD	PD	US2004043389-A1.	
XX	XX	04-MAR-2004.	
XX	PF	04-SEP-2002; 2002US-00235192.	
PR	PR	04-SEP-2002; 2002US-00235192.	
PA	PA	(VITI-) VITIVITY INC.	
PI	PI	Mccarthy J;	
DR	DR	WPI; 2004-214170/20.	
PT	PT	Determining whether a subject has, or is at risk of developing, an	
PT	PT	abnormally low high density lipoprotein-C (HDL-C) level comprises	
PT	PT	detecting an allelic variant of a polymorphic region from any of a set of	
PS	PS	27 genes.	
XX	XX	Disclosure; SEQ ID NO 35; 37pp; English.	
CC	CC	The invention relates to determining whether a subject has, or is at risk	
CC	CC	of developing, an abnormally low high density lipoprotein-C (HDL-C) level	
CC	CC	comprises determining whether the subject has an allelic variant of a	
CC	CC	polymorphic region from any of 27 genes (alleles listed in Table 5 of the	
CC	CC	specification). Also included are determining whether a male subject has,	

or is at risk of developing, an abnormally low HDL-C level, comprising determining whether the male subject has an allelic variant of a polymorphic region listed in Table 5 which is associated with abnormally low HDL-C levels in males, and determining whether a female subject has, or is at risk of developing, an abnormally low HDL-C level, comprising determining whether the female subject has an allelic variant of a polymorphic region listed in Table 5 which is associated with abnormally low HDL-C levels in females. The allelic variant in determining whether a subject has, or is at risk of developing, an abnormally low HDL-C level is APOA 1 CC, CD14 1 CT, COL5A2 1 GG, EDNRB 1 AG or AA, FABP3 1 CT, GGB1 1 AG or GG, LIPC 5 AA, MTHFR 1 CC, VWF 2 GG, or their complements. The allelic variant in determining whether a male subject has, or is at risk of developing, an abnormally low HDL-C level, LRP1 3 CC or CT, PAI2 4 GG, or PPARG 1 CG, or their complements. The allelic variants are also COL5A2 1 GG, CD14 1 CT or CC, and FABP3 1 CT, in combination, or their complements. The methods are useful for diagnosing (a predisposition to) abnormally low levels of low high density lipoprotein-C (HDL-C) in a subject. The methods are useful in diagnosing (a predisposition to) or prognosticating diseases and disorders associated with abnormal lipid levels such as vascular and metabolic diseases, e.g., coronary artery disease. The present sequence is a human gene containing a SNP (single nucleotide polymorphism associated with low high density lipoprotein-C (HDL-C) levels.

Sequence 160361 BP; 43435 A; 35277 C; 35459 G; 45990 T; 0 U; 200 Other;

Query Match	5.9%;	Score 210.6;	DB 12;	Length 160361;
Best Local Similarity	74.8%;	Pred. No. 6.9e-35;		
Matches 264;	Conservative 0;	Mismatches 89;	Indels 0;	Gaps 0;

QY 1057 TTTTAAATTTTTAATTATAATTAATTTGAGTCGTG 1116
||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 152973 TTTGAATTTTAATCTCTTTTTTTTTTTTGAGTCAGTCCG 153032

QY	1117	GCTGTGCGCCAGGCTGAGTGCAGCGCGT	TAATCA	CAGTTCA	CTGCAGCCTCA	ACCTTCT	1176
Db	153033	TTTGTGTGCCAGGCTGAGTGCATATGCA	TATCTCAGATCA	CTGCACCTCCG	CTCCT		153092

Oy 1177 AGGCTCAAGGATTCCTCCCACTCAGCCCCCAAGTAGTTGGGACCAACGATATGCGCA 1236
 Db 153093 GGGTTCAGTGATTCTCTCACTCAGCTTCTCAAGAGCTGGGATTATAGGTGTGCGCCA 153152

Oy 1237 CCATGCTGGCTAATTTCTAATTTTGTAGACATAGGATCTCATATATTGTCAGGC 1296
 |||||
 Db 153153 CCATGCCGGCTAATTTTCCATTTTGTAGTAGGCGCAGGTTTCACCATGTTGGCCAGGC 153212
 |||||

Qy 1297 TGGTCTTGAATTCTCTGGGCTCAGGTGAGCC*CCCACTGGGCTCCCAAGTACTGGGAT 1356
|||||
Db 153213 TGGTCTTGAATTCTCTGAGCTCAAGTATTCACCACTCAGGCTCCCAACTGCTGGGAT 153272

QY 1357 TACAGGCATGAGCCAAAGTCCCTGCCCCATATGAGATTTCCTCTGATCC 1409
|||||
153273 TACAGGCATGAGCCAAAGTCCCTGCCCCATATGAGATTTCCTCTGATCC 153325

RESULT 13
ACN44262
ID ACN44262 standard; DNA; 168821 BP.

DT	18-NOV-2004 (first entry)
XX	
DE	Human genomic sequence hCG18035.

Cytostatic; carcinoma; lymphoma; cancer; human; gene; ss.

Homo sapiens.

XX WO2003073826-A2.
PN
XX
PD 12-SEP-2003.

PF 28-FEB-2003; 2003WO-US006235.
XX
XX 01-MAR-2002; 2002US-00087192.
PR
XX
XX (SAGR-) SAGRES DISCOVERY.
PA
XX
XX Morris DW;
PI
XX
XX WPI; 2003-328604/31.
DR
XX
XX Recombinant nucleic acid useful for diagnosis and treatment of carcinoma
PT comprises a nucleotide sequence.
PT
XX
XX Claim 1; SEQ ID NO 622; Opp; English.
PS
XX
XX The present invention relates to novel DNA and protein sequences which
CC are associated with carcinomas. The sequences are useful for: (i) for
CC screening drug candidates; (ii) for screening of bioactive agent capable
CC of binding to Carcinoma Associated Protein (CAP); (iii) for screening of
CC a bioactive agent capable of modulating the activity of CAP; (iv) for
CC evaluating the effect of a candidate carcinoma drug; (v) for diagnosing
CC carcinoma; (vi) for inhibiting the effect of CAP; (vii) for treating
CC carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biologic;
CC (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for
CC determining Carcinoma Associated (CA) gene copy number. In addition, the
CC CA genes are useful as DNA vaccines and the CAP are useful as markers of
CC carcinoma including lymphoma. The present sequence is one such CA coding
CC sequence. Note: This patent is an equivalent to basic patent
CC US2002182586A1, for which no sequence data was published
CC
XX
SQ Sequence 168821 BP; 39588 A; 43389 C; 45655 G; 40189 T; 0 U; 0 Other;

Query Match 5.9%; Score 210.2; DB 11; Length 168821;
Best Local Similarity 75.6%; Pred. No. 8.6e-35;
Matches 288; Conservative 0; Mismatches 88; Indels 5; Gaps 2;
QY 1008 AGTATTCACCTTGATTGAGACTGGGTAGACAGGTGAAACCATATCAGTTTAAATT 1067
Db 166223 AGAATTGCTTCTCTATTTCTGTCATAAATGGAATCCATGAAATCTATATTAT 166282
QY 1068 TTAATTTTAAATTATTTATTTATTTATTTTGGAGATGAGTCGTGCTG--TCGCC 1125
Db 166283 TTA---TTTATTTATTTATTTATTTATTTTGGAGACGGTCTGTCTATCACC 166339
QY 1126 CAGGCTGAGTGACAGCGCGGTGATCAAGTTCAGCTGACGCTCAACTTCTAGGCTCAG 1185
Db 166340 CAGGCTGAGTACAGTGACAGCAATCTCAGCTCACTGCAACCTCCACCTCCAGGTTCAAG 166399
QY 1186 GGATTCCTCCCACTCAGCCCCCAAGTAGTGGGACCAACGTAATGCGCCACCATGCTG 1245
Db 166400 CGATTCCTCTGCTCAGCCTCCCGAGTAGCTGGGATTACAGGCCACCGCCACGCCCCG 166459
QY 1246 GCTAATTTCTTATTTTGTAGAGATGAGATCTCACTATATTGTCAGGCTGTGTTGA 1305
Db 166460 GCTAATTTTGTATTTTGTAGAGACAGTGTTCACCATGTGGCCAGGCTGTGTTGA 166519
QY 1306 ATTCTGAGCTCAGGTGAGCTCCCACTGGGCTCCCAAGTACTGGGATTACAGGCAT 1365
Db 166520 ACTCTGACCTCAAGGAGATCCGCCCACTCAGCCTCCCAAGTGTGGGATTACAGGCAT 166579
QY 1366 GAGCCAAAGTCCCTGCCCAT 1386
Db 166580 GAGCCAAAGTCCCGGCCCAT 166600

RESULT 14
ABV76540/c
ID ABV76540 standard; cDNA; 1215 BP.
XX
XX ABV76540;
AC
XX
XX 20-FEB-2003 (first entry)
DT
XX

DE Human protein phosphatase 12.76-encoding cDNA.
XX
XX Human; protein phosphatase 12.76; recombinant production; gene therapy;
KW embryonic development disorder; tumour; cancer; cytostatic; gene; ss.
XX
XX Homo sapiens.
OS
XX
XX
FH Key Location/Qualifiers
FT CDS 9..359
FT /*tag= a
FT /product= "Human protein phosphatase 12.76"
FT
XX
XX CN1358852-A.
PN
XX
XX 17-JUL-2002.
PD
XX
XX 13-DEC-2000; 2000CN-00127882.
PF
XX
XX 13-DEC-2000; 2000CN-00127882.
PR
XX
XX (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
PA
XX
XX Mao Y, Xie Y;
PI
XX
XX WPI; 2002-733573/80.
DR
XX
XX P-PSDB; ABP58504.
DR
XX
XX Novel polypeptide-human protein phosphatase 12.76 and polynucleotide for
PT encoding said polypeptide.
PT
XX
XX
PS Claim 6; Page 26-27 (Disclosure); 33pp; Chinese.
XX
XX
CC The invention relates to human protein phosphatase 12.76 (ABP58504) and
CC nucleic acids encoding it (ABV76540). The protein has a molecular weight
CC of 12.76 kD. The invention also relates to a method for the recombinant
CC production of the protein, an antagonist of the protein, and the use of
CC the protein, gene and antagonist in therapeutic applications. Protein
CC phosphatase 12.76 can be used in the treatment of a variety of diseases
CC such as embryonic development disorders and tumours. The present sequence
CC represents cDNA encoding human protein phosphatase 12.76
CC
SQ Sequence 1215 BP; 345 A; 276 C; 281 G; 313 T; 0 U; 0 Other;

Query Match 5.9%; Score 210; DB 6; Length 1215;
Best Local Similarity 76.3%; Pred. No. 1.9e-35;
Matches 258; Conservative 0; Mismatches 80; Indels 0; Gaps 0;
QY 1064 TTTTAAATTTTAAATTTATTTATTTATTTATTTTGGAGTAGAGTCTGCTGCTCG 1123
Db 823 TTTTAAATTTTATTTATTTATTTATTTATTTATTTTGGAGACAGGCTCACTCTGTC 764
QY 1124 CCGAGCTGAGTGACAGCGCGGTGATCAAGTTCAGTCACTGACGCTCAACCTTCTAGGCTCA 1183
Db 763 CCGAGCTGAGTGACAGTGACAGCAATCATAGCTCACTGACGCTTGACCTCCAGACTCA 704
QY 1184 AGGATTCCTCCCACTCAGCCCCCAAGTAGTGGGACCAACGTAATGCGCCACCATGCC 1243
Db 703 AGCGATCTCCCATCTTAGCTTCCAGCAGCTGGGATTACAGGTGTATGCCACCATGCC 644
QY 1244 TGGCTAATTTCTTATTTTGTAGAGATGAGATCTCACTATAATGTGCCAGGCTGTCTT 1303
Db 643 TGGTAAAGTTTAAATTTATTTGTAGAGATGAGGCTCACTGTGTGCCAGGCTGTCTC 584
QY 1304 GAATTCCTGGGCTCAGGTGAGCTCCCACTGGGCTCCCAAGTACTGGGATTACAGGC 1363
Db 583 CAATCTCTGGGCTCAAGTATCTCCCGCTCAGCCTCCCAAGTGTGGGATTACAGGT 524
QY 1364 ATGAGCAAGTCCCTGCGCATATGAGATTTCTGTC 1401
Db 523 GTGAGCACTGCACTCAGTCGGGAAGCCCTTCTAATTC 486

RESULT 15

ABZ74119/c
ID ABZ74119 standard, DNA; 10554 BP.
XX
AC ABZ74119;
XX
DT 12-MAY-2003 (first entry)
XX
DE Secreted protein gene 184 genomic fragment HLMBB73, SEQ ID NO:1266.
XX
KW Human; secreted protein; cancer; tumour; hyperproliferative disorder;
KW autoimmune disorder; inflammation; angiogenic diseases; AIDS;
KW acquired immunodeficiency syndrome; hepatitis; anaemia; wound healing;
KW drug screening; chromosome identification; chromosome mapping;
KW cytostatic; gene therapy; antiinflammatory; immunomodulator; anti-HIV;
KW antianaemic; vulnerary; gene; ds.
XX
OS Homo sapiens.
XX
PN WO200277013-A2.
XX
PD 03-OCT-2002.
XX
PF 26-MAR-2002; 2002WO-US009370.
XX
PR 27-MAR-2001; 2001US-0278650P.
PR 12-SEP-2001; 2001US-00950082.
PR 12-SEP-2001; 2001US-00950083.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI; 2003-040578/03.
XX
PT New human secreted proteins and nucleic acids, useful for detecting or
PT treating cancer or other hyperproliferative disorders, autoimmune
PT disorders, inflammatory disorders, HIV disease, hepatitis or anemia.
XX
PS Disclosure; Page 1899-1901; 2474pp; English.
XX
CC ABZ73281-ABZ73697 represent cDNAs corresponding to 391 human secreted
CC protein genes, and ABP00947-ABP01363 represent the proteins they encode.
CC ABZ73698-ABZ74687 represent human secreted protein genomic fragments. The
CC invention also encompasses antibodies specific for the secreted proteins,
CC the use of the secreted proteins in drug screening and recombinant
CC vectors and host cells comprising a nucleic acid of the invention. The
CC secreted proteins are thought to be involved in biological activities
CC associated with cellular signalling, cellular differentiation, cell
CC migration, prohormone activation and neurotransmitter activity. The
CC secreted proteins, nucleic acids encoding them, antibodies or antibody
CC fragments specific for the secreted proteins, and modulators of protein
CC activity are useful for diagnosing or treating cancers or other
CC hyperproliferative disorders. Additionally, the secreted proteins and
CC their nucleic acids may also be used in the treatment of autoimmune
CC disorders, inflammatory disorders, diseases involving angiogenesis, AIDS
CC (acquired immunodeficiency syndrome), hepatitis, anaemia, and to promote
CC wound healing. Nucleic acids of the invention may be used for chromosome
CC identification, chromosome mapping, in gene therapy, for identifying
CC individuals from minute biological samples, as hybridisation probes, and
CC as molecular weight markers. The present sequence represents a human
CC secreted protein genomic fragment referred to in the disclosure of the
CC invention
XX
SQ Sequence 10554 BP; 3162 A; 1831 C; 2038 G; 3523 T; 0 U; 0 Other;

Query Match 5.9%; Score 209.8; DB 8; Length 10554;
Best Local Similarity 76.9%; Pred. No. 4.2e-35;
Matches 256; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

Qy 1068 TTAATTTTAAATTAATTATTATTATTATTTTGGAGAGGAGTCTGGCTGCGCCCA 1127
Db 3224 TTTAGTCTTATTATTAGGATATTTATTATTATTAGATGAGTCTGCTGCACCCA 3165

Qy 1128 GGCTGAGTGACGCGCGGTGATCACAGTTCACTGCAAGCTCAACCTTCTAGGCTCAAGG 1187
Db 3164 GGCTGAGTGACAGTGGACAATCTCAGCTCACTGCAACCTCCGCTCCTAGGTTCAAGCA 3105
Qy 1188 ATTCTCCCACTCAGCGCCCAAGTAGTTGGACCAACGATGCGCCACCATGCTGGC 1247
Db 3104 ATTCTCTGTCTCAGCATGCGAGTAGCTGGGATTACAGGCATGCGCCACCATGTCAGC 3045
Qy 1248 TAAATTCCTATTTTGTAGAGATAGATCTCACTAATTTGTCAGGCTGCTTGAAT 1307
Db 3044 TAAATTTTGCAATTTTAGTAGAGATGGTTTTCACCAATGTGGCCAGGCTGACTGCAAC 2985
Qy 1308 TCCTGGGCTCAGGTGAGCCTCCCACTGGGCTCCCAAGTACTGGATTACAGGATGA 1367
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Db 2924 GCCACTGTCCCAAGCCATTTTAGGGATTTTAT 2892

Search completed: January 7, 2006, 07:04:56
Job time : 1965.21 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 7, 2006, 05:41:27 ; Search time 17670.5 Seconds
(without alignments)
11535.651 Million cell updates/sec

Title: US-10-767-521-3

Perfect score: 3586

Sequence: 1 ggcacccctacctcccatc.....ctatcacaggagagtga 3586

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

- GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
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11: gb_sy:*
12: gb_un:*
13: gb_vi:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	3586	100.0	3586	6	AR164120	AR164120 Sequence
2	3586	100.0	3586	6	BD128570	BD128570 Bosinophi
3	3586	100.0	3586	6	AX030930	AX030930 Sequence
4	3494.4	97.4	5791	6	AX705064	AX705064 Sequence
5	3494.4	97.4	5791	8	AF247361	AF247361 Homo sapi
6	3494.4	97.4	177334	8	AC138069	AC138069 Homo sapi
7	3492.8	97.4	197279	8	AC104439	AC104439 Homo sapi
8	3481.6	97.1	220965	14	HSA312688	AJ312688 Homo sapi
9	3408.6	95.1	7010	8	AF224497	AF224497 Homo sapi
10	3388	94.5	3388	8	AF237381	AF237381 Homo sapi
11	2406	67.1	7201	6	AX345239	AX345239 Sequence
12	2271.8	63.4	7201	6	AX345238	AX345238 Sequence
13	1066.2	29.7	1310	8	AF262300	AF262300 Homo sapi
14	358.6	10.0	436	8	AF262304	AF262304 Homo sapi
15	344.2	9.6	1915	6	ARS84940	ARS84940 Sequence
16	344.2	9.6	1915	6	BD006761	BD006761 Chemokine
17	344.2	9.6	1915	6	BD017703	BD017703 Chemokine
18	308.8	8.6	167298	4	AP006436	AP006436 Sus scrof

19	219.8	6.1	112967	8	AC025177	AC025177 Homo sapi
20	218.2	6.1	123551	8	AC026361	AC026361 Homo sapi
21	218.2	6.1	131329	8	AC004873	AC004873 Homo sapi
22	218.2	6.1	157435	8	HS50024	AL034380 Human DNA
23	217.8	6.1	146740	8	CNS01DTX	AL132989 Human chr
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25	217	6.1	151846	8	AP001630	AP001630 Homo sapi
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45	212.6	5.9	123708	8	HS190A9	AJ006997 Homo sapi

ALIGNMENTS

RESULT 1
AR164120
LOCUS AR164120 3586 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 3 from patent US 6271347.
ACCESSION AR164120
VERSION AR164120.1 GI:16235066
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3586)
AUTHORS Daugherty,B.L., Demartino,J.A., Siciliano,S.J. and Springer,M.S.
TITL E Bosinophil eotaxin receptor
JOURNAL Patent: US 6271347-A 3 07-AUG-2001;
FEATURES
source Location/Qualifiers
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ORIGIN

Query Match	100.0%;	Score 3586;	DB 6;	Length 3586;
Best Local Similarity	100.0%;	Pred. No. 0;		
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QY	1	GGATCCCTACCTTCCCGACAGAGCTAGGGGCGCATGGAGCGCTCTGTGCTAAGATGGGA	60	
Db	1	GGATCCCTACCTTCCCGACAGAGCTAGGGGCGCATGGAGCGCTCTGTGCTAAGATGGGA	60	
QY	61	CCCCCAAGATGTCTCCCTGTGGGGCACTTCCTTACCAAGATGGGCGGCTT	120	
Db	61	CCCCCAAGATGTCTCCCTGTGGGGCACTTCCTTACCAAGATGGGCGGCTT	120	
QY	121	AAGTTGTGTGTCAGGCGAAGAAAAAGATCTAGTTTGTACTCTTGAGAGTTCTCGGTTT	180	
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QY	181	GTTTCATGGCATGGGCGAGGAGTCAAGAGGACGAGGCTTGCCTCAGTGCTTACCACTGCA	240	
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RESULT 2
BD128570 3586 bp DNA linear PAT 18-SEP-2002
LOCUS BD128570
DEFINITION Bosinophil eotaxin receptor.
ACCESSION BD128570
VERSION BD128570.1 GI:23223515
KEYWORDS JP 2002503950-A/2.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 3586)
AUTHORS Daugherty, B.L., Demartino, J.A., Springer, M.S. and Siciliano, S.J.
TITLE Bosinophil eotaxin receptor
JOURNAL Patent: JP 2002503950-A 2 05-FEB-2002;
MERCK & CO INC
COMMENT OS Unidentified
PN JP 2002503950-A/2
PD 05-FEB-2002
PF 24-APR-1997 JP 1997538970
PR 26-APR-1996 US 08/640991, 26-APR-1996 US 60/016158 PR
17-JAN-1997 GB 9700894.0
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'SALVATORE J SICILIANO
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CC Strandedness: Single;
CC Topology: Linear;
CC Bosinophil eotaxin receptor
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ORIGIN
Query Match 100.0%; Score 3586; DB 6; Length 3586;
Best Local Similarity 100.0%; Pred. No; 0;
Matches 3586; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	781	GTTGACCTCATTTGTAAATCTTGACACACGGGGCAATCCAATATCTGCACAAGAGATATG	840
Db	781	GTTGACCTCATTTGTAAATCTTGACACACGGGGCAATCCAATATCTGCACAAGAGATATG	840
Qy	841	TTAACCACTGTTAAATGCTGCATGAGGAGATTGGGTGATTTTACTTTCGTTTGTGCT	900
Db	841	TTAACCACTGTTAAATGCTGCATGAGGAGATTGGGTGATTTTACTTTCGTTTGTGCT	900
Qy	901	CTTCTTCTTATTTGTTCTTACTTATTTACGATTACCTTATCTGTTTCCCAAAATGTAAAA	960
Db	901	CTTCTTCTTATTTGTTCTTACTTATTTACGATTACCTTATCTGTTTCCCAAAATGTAAAA	960
Qy	961	GGCCATTTTGAAAGCCTAATTCAAAACCTCTTCACTAATTTGTATCTAAGTATTACCTTG	1020
Db	961	GGCCATTTTGAAAGCCTAATTCAAAACCTCTTCACTAATTTGTATCTAAGTATTACCTTG	1020
Qy	1021	ATTGAGACTGGGTAGACAGGTGAAAAACCATATCAGGTTTTTAATTTTAAATTTTAAAT	1080
Db	1021	ATTGAGACTGGGTAGACAGGTGAAAAACCATATCAGGTTTTTAAATTTTAAATTTTAAAT	1080
Qy	1081	ATTTATTTATTTATTTATTTTGTGAGATGAGTCTGGCTGTGCCCAAGGCTGAGTGCAG	1140
Db	1081	ATTTATTTATTTATTTATTTTGTGAGATGAGTCTGGCTGTGCCCAAGGCTGAGTGCAG	1140
Qy	1141	CGGCGTGATCACAGTTCACCTGCAGCCTCAACCTTCTAAGCTCAAGGATTCCTCCACCTC	1200
Db	1141	CGGCGTGATCACAGTTCACCTGCAGCCTCAACCTTCTAAGCTCAAGGATTCCTCCACCTC	1200
Qy	1201	AGCCCCCAAGTAGTTGGGACCAACAGTATGCGCCACCATGCTGGCTAATTTCTTAATTT	1260
Db	1201	AGCCCCCAAGTAGTTGGGACCAACAGTATGCGCCACCATGCTGGCTAATTTCTTAATTT	1260
Qy	1261	TTTTGTAGAGATAGGATCTCATATATTGTCCAAGCTGGTCTTGAATTCCTGGGCTCAGG	1320
Db	1261	TTTTGTAGAGATAGGATCTCATATATTGTCCAAGCTGGTCTTGAATTCCTGGGCTCAGG	1320
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Qy	1381	GCCCATATGAGATTTTCTGTCTCTGATCCCATGCAAGTATCAAGGACTTGGCTGCT	1440
Db	1381	GCCCATATGAGATTTTCTGTCTCTGATCCCATGCAAGTATCAAGGACTTGGCTGCT	1440
Qy	1441	GACTCTGAGGACCTGCATGCTTTCTTGAGCTGTGAACCTTCAAGTCTAAAAAGCTCATAGG	1500
Db	1441	GACTCTGAGGACCTGCATGCTTTCTTGAGCTGTGAACCTTCAAGTCTAAAAAGCTCATAGG	1500

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Db	1501	CAGCCCTGAAACCCBAACCAAAAGTTCTATGGTTTATCATCTGATCATGTTGATTTTA	1560
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QY	1861	TGATGGAGCACACAAACCATTGTTCTCAGTCCATTTCCTCCTCAAAAGCCTGGA	1920
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Db	1921	ATGTGCCATTGATCAGTGGGAGATGTAACCTGACAGACCATGAAAAAGATCAACAAGT	1980
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Db	2281	CCTCAGTATTCGATCAATTATTTCTATTAAAGCAAAAACAATTCCCCGCATTGGCCCCA	2340
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Db	2401	TTCAACCCTGTCCCTTCTCTAGAAAGGAGAAAGTCAGTTGATGCCCCCTGAGGAACCT	2460
QY	2461	AGTGCATGGCTTAACGTCTTCCATGACTCCTGCTTATCTGTTTCTATTTTCTCTCT	2520
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Db 2581 AGAATATCAAGTCCAGTAGAAGATCCCATGACTGACCCCTCTGCTTAACCCCTTGTG 2640

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RESULT 3
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LOCUS AX030930
DEFINITION Sequence 3 from Patent BP1012190.
ACCESSION AX030930

VERSION AX030930.1 GI:10278335
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Daugherty, B.L., Demartino, J.A., Siciliano, S.J. and Springer, M.S.
TITLE Eosinophil eotaxin receptor
JOURNAL Patent: EP 1012190-A 3 28-JUN-2000;
MERCK & CO INC (US)
FEATURES
Source location/Qualifiers
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 3586; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GGATCCCTAACCTTCCCATCAAGCTAGGGGGCATGAGCGCTCTGCTAAGATGGGA 60

Qy 61 CCCCCAAGAAATGCTCTCCCTGTGGGCACTTCCTTACCAAGATGGGAGTGGGCTT 120

Db 61 CCCCCAAGAAATGCTCTCCCTGTGGGCACTTCCTTACCAAGATGGGAGTGGGCTT 120

Qy 121 AAGTTGTGTGTCAGGCAAGAAAGAAAGATCTAGTTGTACTCTGAGAGTTCTCGGTTT 180

Db 121 AAGTTGTGTGTCAGGCAAGAAAGAAAGATCTAGTTGTACTCTGAGAGTTCTCGGTTT 180

Qy 181 GTTCATGGCATGGGCAAGAGTCAAGAGCAGCAGCTTGCCTCAAGTCAAGTCA 240

Db 181 GTTCATGGCATGGGCAAGAGTCAAGAGCAGCAGCTTGCCTCAAGTCAAGTCA 240

Qy 241 GGAAGAGTGCATAGCTGGGCGCAGGCGCCAGGCGCTGTGTGAGGCGTAGTGTAACAGA 300

Db 241 GGAAGAGTGCATAGCTGGGCGCAGGCGCCAGGCGCTGTGTGAGGCGTAGTGTAACAGA 300

Qy 301 GAGGCTCTCCATTCCAGCCCAAGAGAGCTAAGAAATGAATTAATCTCATGATATTAATG 360

Db 301 GAGGCTCTCCATTCCAGCCCAAGAGAGCTAAGAAATGAATTAATCTCATGATATTAATG 360

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Qy 421 TCAGAGACACAGTCAATATAATCAAGAACCAACAGAGACAGAAACACCCCTTCCCA 480

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RESULT 4
LOCUS AX705064 5791 bp DNA linear PAT 04-APR-2003
DEFINITION Sequence 5 from Patent WO03014153.
ACCESSION AX705064
VERSION AX705064.1 GI:29561706
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
1 Renzl, P., Zemzoumi, K. and lamkhioned, B.
TITLE Cellular virus receptors and methods of use
JOURNAL Patent: WO 03014153-A 5 20-FEB-2003;
Topigen Pharmaceutical Inc (CA)
FEATURES
source location/Qualifiers
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DEFINITION	Homo sapiens	CC chemokine receptor 3 (CCR3) gene, complete cds.					
ACCESSION	AF247361						
VERSION	AF247361.1	GI:19110542					

SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens

REFERENCE	
AUTHORS	
1	(bases 1 to 5791)
Vijh, S., Dayhoff, D.B., Wang, C.B., Imam, Z., Ehrenberg, P.K. and Michael, N.L.	

TITLE	Transcription Regulation of Human Chemokine Receptor CCR3: Evidence for a Rare TATA-less Promoter Structure Conserved between
JOURNAL	Drosophila and Humans
PUBMED	Genomics 80 (1), 86-95 (2002)
REFERENCE	12079287
AUTHORS	2 (bases 1 to 5791)
TITLE	Vijh, S., Dayhoff, D.E., Wang, C.B., Ehrenberg, P.K. and Michael, N.L.
JOURNAL	Direct Submission
	Submitted (21-MAR-2000) Dept. of Mol. Diag. and Pathogenesis, U.S.
	Military HIV Research Program, 1600 E. Gude Drive, Rockville, MD
	20850, USA

FEATURES	
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Db 2587 AGTAAAGGAGGCTCTGCATTTAAGGGCTTGTCCAAGGCAACGACCTGAGAGGCGCTAGAC 2646

QY 2220 TGGCTCCATTTCCATCTATTTCTCACTGACCTTTGACTAACCCAGAACCCCAACATGTGGG 2279
| | | | |
Db 2647 TGGCTCCATTTCCATCTATTTCTCACTGACCTTTGACTAACCCAGAACCCCAACATGTGGG 2706

QY 2280 GCGTCAGTATTCGATCAATTATTTCTATTAAGAGCAAAACAATTCGCCGATTTGGCCCC 2339
| | | | |
Db 2707 GCGTCAGTATTCGATCAATTATTTCTATTAAGAGCAAAACAATTCGCCGATTTGGCCCC 2766

QY 2340 AGTTATTAAGCATTTCTCAGATTTTACCTTGAGAAATGCCATCGGCTGTATATTGCAT 2399
| | | | |
Db 2767 AGTTATTAAGCATTTCTCAGATTTTACCTTGAGAAATGCCATCGGCTGTATATTGCAT 2826

QY 2400 CTTCAACCTTGTCCCTTCTCTCTAGAAAAGAGAAAGTCAAGTTGATGCCCTCTGAGGAAC 2459
| | | | |
Db 2827 CTTCAACCTTGTCCCTTCTCTCTAGAAAAGAGAAAGTCAAGTTGATGCCCTCTGAGGAAC 2886

QY 2460 TAGTGATGGCTTAACTGTCTTCCATGACTCTGCTTATCTGTTTCTATTTTCTCTCC 2519
| | | | |
Db 2887 TAGTGATGGCTTAACTGTCTTCCATGACTCTGCTTATCTGTTTCTATTTTCTCTCC 2946

QY 2520 TTTTCCACCGAAGTCTAATACTCAAGAAAAGCAGGCACTGGCCTTAGGGCTCCTGGCCT 2579
| | | | |
Db 2947 TTTTCCACCGAAGTCTAATACTCAAGAAAAGCAGGCACTGGCCTTAGGGCTCCTGGCCT 3006

QY 2580 AAGAAATATCAAGTCCAGTGAGAAATCCCATTTGACTGAACCCCTCTGCTTACCCTTTGT 2639
| | | | |
Db 3007 AAGAAATATCAAGTCCAGTGAGAAATCCCATTTGACTGAACCCCTCTGCTTACCCTTTGT 3066

QY 2640 GATGAGAAAGCTCCAGGGGTTTGTCTTTTGCACTGTACCAAGGCTTAACCTCAGCATCAC 2699
| | | | |
Db 3067 GATGAGAAAGCTCCAGGGGTTTGTCTTTTGCACTGTACCAAGGCTTAACCTCAGCATCAC 3126

QY 2700 AGGGCAAGAAAAAGAAAGTAACCTAACTAATGCTGCTTATAATTGTAATTATTGTAAT 2759
| | | | |
Db 3127 AGGGCAAGAAAAAGAAAGTAACCTAACTAATGCTGCTTATAATTGTAATTATTGTAAT 3186

QY 2760 AGTTAATTACTGTGATTGTACATGTGTAAACAGACAAAATGTGTATTTTTCACAGCTGC 2819
| | | | |
Db 3187 AGTTAATTACTGTGATTGTACATGTGTAAACAGACAAAATGTGTATTTTTCACAGCTGC 3246

QY 2820 TGTGATTGGATTATGCCATTTGGAATTAAGAAATGCTGTTAAGACACACAAGCCAAGTTC 2879

Db	Accession	Sequence	Length
Db	3247	TGTGGATTGGATTATGCCATTGTGGAATAGATGCTGTTAAGAGCACACAGCCAGGTTCC	3306
Qy	2880	CTCAAGTCCGTAGCAAATTTTTCAAAAGTTAAATTTAATAATCACTACATTTGAATCTAG	2939
Db	3307	CTCAAGTCCGTAGCAAATTTTTCAAAAGTTAAATTTAATAATCACTACATTTGAATCTAG	3366
Qy	2940	TGACAGAGAAATGGAATGATGATAGAGACTTAAAGATCTAGCCCAAATTTTATATTAATCTT	2999
Db	3367	TGACAGAGAAATGGAATGATGATAGAGACTTAAAGATCTAGCCCAAATTTTATATTAATCTT	3426
Qy	3000	GTTAGAGATTGTAACAAATTAATAATTTCTTCAAGGTTCAATTTCCCATTAATCTAT	3059
Db	3427	GTTAGAGATTGTAACAAATTAATAATTTCTTCAAGGTTCAATTTCCCATTAATCTAT	3486
Qy	3060	AATGAATGCTCATCATTAATGAGGCCCCCTGAGAGACATTAATTAATCTGTATTTGTAATAT	3119
Db	3487	AATGAATGCTCATCATTAATGAGGCCCCCTGAGAGACATTAATTAATCTGTATTTGTAATAT	3546
Qy	3120	CATTGTTATTTATTAATTAATTAATTAATTTGCTTTTAAATGATTAAGATTTTAAAGTATAT	3179
Db	3547	CATTGTTATTTATTAATTAATTAATTAATTTGCTTTTAAATGATTAAGATTTTAAAGTATAT	3606
Qy	3180	GTTAACTGTAAACATTAATAATGCAAAATGCCCCGTAAGAGACAGTAGTAATAATAATGATTA	3239
Db	3607	GTTAACTGTAAACATTAATAATGCAAAATGCCCCGTAAGAGACAGTAGTAATAATAATGATTA	3666
Qy	3240	TTATATTGTTATCATTAATTAATTAATGCTGTTTTCCTGTTGTTGTTATTTCTTCTTAAATGC	3299
Db	3667	TTATATTGTTATCATTAATTAATTAATGCTGTTTTCCTGTTGTTGTTATTTCTTCTTAAATGC	3726
Qy	3300	TTACAGAAATCTGTATCCCATTTCTTACACACACACCCACAACATTTCTGCTTCTTCC	3359
Db	3727	TTTACAGAAATCTGTATCCCATTTCTTACACACACACCCACAACATTTCTGCTTCTTCC	3786
Qy	3360	CATGCC-GGTTCATGCTTAATCTTGAAGCTTCAGCTCTTCTTCTTCTTCTTCTTCTG	3418
Db	3787	CATGCCGGGTTCATGCTTAATCTTGAAGCTTCAGCTCTTCTTCTTCTTCTTCTTCTG	3846
Qy	3419	GCACCTCTGATATGCTTTTGAATAATCATGTTAAAGAAATCCCTAGGCTGCTATCACATGT	3478
Db	3847	GCACCTCTGATATGCTTTTGAATAATCATGTTAAAGAAATCCCTAGGCTGCTATCACATGT	3906
Qy	3479	GGCATCTTGTGTTGATGATGATGAATAATCAACTGGTGTGTTTGAAGAGATGATTAATGC	3538
Db	3907	GGCATCTTGTGTTGATGATGATGAATAATCAACTGGTGTGTTTGAAGAGATGATTAATGC	3966
Qy	3539	TTCAATTGTGGATTGTAATTTTCTTCTTCTATCACAGGAGAGATGAA	3586
Db	3967	TTCAATTGTGGATTGTAATTTTCTTCTTCTATCACAGGAGAGATGAA	4014
RESULT 6			
AC138069	177334 bp	DNA linear	PRI 19-FEB-2003
LOCUS	AC138069	Homo sapiens chromosome 3 clone RP13-54612, complete sequence.	
DEFINITION	AC138069		
ACCESSION	AC138069.3	GI:28416170	
VERSION			
KEYWORDS	HTG.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;		
	Homnidae; Homo.		
REFERENCE	1 (bases 1 to 177334)		
AUTHORS	Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,		
	Saenphimachak, C., Buckley, D., Kibukawa, M., Raymond, C. and		
	Haugen, B.D.		
	Direct Submission		
	Unpublished		
	2 (bases 1 to 177334)		
	Kaul, R.K., Olson, M.V., Raymond, C. and Haugen, B.D.		
	Direct Submission		

JOURNAL	Submitted (12-DEC-2002) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA
REFERENCE	3 (bases 1 to 177334)
AUTHORS	Kaul, R.K., Olson, M.V., Raymond, C. and Haugen, E.D.
TITLE	Direct Submission
JOURNAL	Submitted (10-JAN-2003) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA
REFERENCE	4 (bases 1 to 177334)
AUTHORS	Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z., Saenphimmachak, C., Buckley, D., Kibukawa, M., Raymond, C. and Haugen, E.D.
TITLE	Direct Submission
JOURNAL	Submitted (19-FEB-2003) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA
COMMENT	On Feb 19, 2003 this sequence version replaced gi:27573398.

Direct Submission
 Submitted (19-FEB-2003) Genome Center, University of Washington,
 Box 352145, Seattle, WA 98195, USA
 On Feb 19, 2003 this sequence version replaced gi:27573398.
 ----- Genome Center -----
 Center: University of Washington Genome Center
 Center Code: UWGC
 Web site: <http://www.genome.washington.edu>
 Contact: uwgchgs@u.washington.edu
 ----- Project Information -----
 Center project name: chr-3
 Center clone name: RP13-54612 (bc0820)
 ----- Summary Statistics -----
 Sequencing vector: plasmid; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.990319
 Consensus quality: 177210 bases at least Q40
 Consensus quality: 177313 bases at least Q30
 Consensus quality: 177334 bases at least Q20
 Insert size: 177334; sum-of-contigs
 Quality coverage: 9.3x in Q20 bases; sum-of-contigs

Overlapping Sequences:
 5': RP11-793B15 (UWGC:bc0504) AC104439, 95469-bp overlap
 3': U95626, 42710-bp overlap

Sequence Quality Assessment: This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp. Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality ≥ 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

Sequence Validation: This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

Fingerprints are separated by uncode lines.			
HindIII	ECORI	BglII	
SeqDerMap	FngRPrnt	SeqDerMap	FngRPrnt
-----	-----	-----	-----
1239	1199	11125	10952
-----	-----	-----	-----
		6306	6319

-----	-----	-----	-----	-----	-----
449	<800	2290	2310	2067	2071
-----	-----	-----	-----	-----	-----
510	<800	560	<800	3913	3756
-----	-----	-----	-----	-----	-----
6511	6363	54	<800	2169	2210
-----	-----	-----	-----	-----	-----
5296	5509	1159	1158	910	910
-----	-----	-----	-----	-----	-----
10424	10027	4052	4034	875	883
-----	-----	-----	-----	-----	-----
5046	5119	1846	1829	3716	3756
-----	-----	-----	-----	-----	-----
1196	1199	8334	8273	4502	4523
-----	-----	-----	-----	-----	-----
1397	1392	12882	12573	1967	1945
-----	-----	-----	-----	-----	-----
2597	2624	448	<800	2864	2871
-----	-----	-----	-----	-----	-----
1688	1674	12737	12573	4724	4738
-----	-----	-----	-----	-----	-----
3800	3818	10300	10103	4773	4738
-----	-----	-----	-----	-----	-----
2248	2269	6671	6656	3707	3756
-----	-----	-----	-----	-----	-----
1074	1055	4052	4034	336	<800
-----	-----	-----	-----	-----	-----
7303	7718	1392	1386	79	<800
-----	-----	-----	-----	-----	-----
959	959	4253	4286	4736	4738
-----	-----	-----	-----	-----	-----
551	<800	2791	2834	1889	1945
-----	-----	-----	-----	-----	-----
1074	1055	2647	2682	3696	3756
-----	-----	-----	-----	-----	-----
5688	5759	3423	3409	1569	1539
-----	-----	-----	-----	-----	-----
5183	5363	73	<800	8078	8038
-----	-----	-----	-----	-----	-----
3100	3093	499	<800	1365	1325
-----	-----	-----	-----	-----	-----
921	959	723	<800	289	<800
-----	-----	-----	-----	-----	-----
4350	4244	2763	2834	11047	10790
-----	-----	-----	-----	-----	-----
4931	4857	6594	6656	8848	8963
-----	-----	-----	-----	-----	-----
3907	3818	4503	4468	1914	1945
-----	-----	-----	-----	-----	-----
8001	7718	5154	5136	1336	1325
-----	-----	-----	-----	-----	-----
3804	3818	4730	4713	11485	11341
-----	-----	-----	-----	-----	-----
2355	2376	13628	13324	974	975
-----	-----	-----	-----	-----	-----
862	868	166	<800	2448	2501
-----	-----	-----	-----	-----	-----
1711	1674	9554	9494	373	<800
-----	-----	-----	-----	-----	-----
5672	5759	1398	1386	1003	975
-----	-----	-----	-----	-----	-----
3900	3818	1613	1641	1787	1756
-----	-----	-----	-----	-----	-----
1905	1854	1479	1503	857	883
-----	-----	-----	-----	-----	-----
7872	7718	1540	1503	1974	1945
-----	-----	-----	-----	-----	-----
1174	1155	520	<800	1707	1631
-----	-----	-----	-----	-----	-----
7015	7139	219	<800	3835	3756
-----	-----	-----	-----	-----	-----
2852	2868	1571	1503	6586	6551
-----	-----	-----	-----	-----	-----

-----	221	<800	154	<800	178	<800
-----	-----	-----	-----	-----	-----	-----
-----	1002	1055	5077	5136	2905	2871
-----	-----	-----	-----	-----	-----	-----
-----	201	<800	2156	2190	2500	2501
-----	-----	-----	-----	-----	-----	-----
-----	6717	6864	1075	1089	389	<800
-----	-----	-----	-----	-----	-----	-----
-----	237	<800	162	<800	41	<800
-----	-----	-----	-----	-----	-----	-----
-----	2737	2749	2752	2834	685	<800
-----	-----	-----	-----	-----	-----	-----
-----	3448	3416	1647	1641	2598	2662
-----	-----	-----	-----	-----	-----	-----
-----	3256	3238	7059	7056	248	<800
-----	-----	-----	-----	-----	-----	-----
-----	5801	5759	1547	1503	2152	2210
-----	-----	-----	-----	-----	-----	-----
-----	1512	1497	5163	5136	431	<800
-----	-----	-----	-----	-----	-----	-----
-----	1398	1392	8679	8719	237	<800
-----	-----	-----	-----	-----	-----	-----
-----	8413	8333	2033	2035	3380	3411
-----	-----	-----	-----	-----	-----	-----
-----	6621	6614	886	892	5694	5744
-----	-----	-----	-----	-----	-----	-----
-----	645	<800	-----	-----	3255	3265
-----	-----	-----	-----	-----	-----	-----
-----	1026	1055	-----	-----	183	<800
-----	-----	-----	-----	-----	-----	-----
-----	14333	14484	-----	-----	3128	3144
-----	-----	-----	-----	-----	-----	-----
-----	-----	-----	-----	-----	10701	10790
-----	-----	-----	-----	-----	1321	1325

Query Match 97.4%; Score 3494.4; DB 8; length 177334;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 3569; Conservative 0; Mismatches 11; Indels 8; Gaps 6;

QY	1	GGATCCCTA	CCTCCCATCAGAGCTAGGGG	GCATGAGCGCTCTGTAGATGGGA	60
DB	84809	GGATCCCTA	CCTCCCATCAGAGCTAGGGG	GCATGAGCGCTCTGTAGATGGGA	84868
QY	61	CCCCAAGA	TGTCCTCTGTGGGCACTTCCTT	ACAGATGGATGGCAGTGGGTT	120
DB	84869	CCCCAAGA	TGTCCTCTGTGGGCACTTCCTT	ACAGATGGATGGCAGTGGGTT	84928
QY	121	AAGTGTGT	GTCAGGCAGAAAAAAGATCTA	GTGTGTACTTGAAGTTCCTCGTTT	180
DB	84929	AAGTGTGT	GTCAGGCAGAAAAAAGATCTA	GTGTGTACTTGAAGTTCCTCGTTT	84988
QY	181	GTTCATGG	CATGGGCAAGTCAAGACAGACCTT	GCTCAGTGCCCTACCAAGTGA	240
DB	84989	GTTCATGG	CATGGGCAAGTCAAGACAGACCTT	GCTCAGTGCCCTACCAAGTGA	85048
QY	241	GGAAAGST	GATAGCCTGGGCCAGGGCCAGGG	CCCTGTGTGAGGCGTAGTGTAA	300
DB	85049	GGAAAGST	GATAGCCTGGGCCAGGGCCAGGG	CCCTGTGTGAGGCGTAGTGTAA	85108
QY	301	GAGGGCTT	CTCATTTCCAGGCCCAAGAGACTA	GAATGAATACCTCATGATATTA	360
DB	85109	GAGGGCTT	CTCATTTCCAGGCCCAAGAGACTA	GAATGAATACCTCATGATATTA	85168
QY	361	TACAAACA	CCACAGCAGGTTCCAGAAAAAGG	CTCAGCGTTGAAACAGGTCA	420
DB	85169	TACAAACA	CCACAGCAGGTTCCAGAAAAAGG	CTCAGCGTTGAAACAGGTCA	85228
QY	421	TCAGGACA	CCAGTCAATATAATCAAGACCA	ACAGAGACAGAAACCCCTTCCA	480
DB	85229	TCAGGACA	CCAGTCAATATAATCAAGACCA	ACAGAGACAGAAACCCCTTCCA	85288
QY	481	CTTGCCCC	ATGTCTCAAGTTGTAGTGCCCTT	CCTCCAGATCTGTGCCACCAT	CTTAGA 540

Db 85289 CTTGCCCCATGTCTCAAGTTGTATGGCCCCCTTCTCCAGATCTCTGCCACCATCTTAGA 85348
Qy 541 AAGGAACA CTGAAAGAGAACTGAAATTATTAAGCTGACAGCATTAAGAAGATGAGTAA 600
Db 85349 AAGGAACA CTGAAAGAGAACTGAAATTATTAAGCTGACAGCATTAAGAAGATGAGTAA 85408
Qy 601 ACCTTAAATCATTTGTTCAATGAATGAATCAAGAGAAGTTTAAACCACTTTGACTTAAA 660
Db 85409 ACCTTAAATCATTTGTTCAATGAATGAATCAAGAGAAGTTTAAACCACTTTGACTTAAA 85468
Qy 661 TGTGTGAATCCTTTTTCCTGCTATCCAGCAGATGAGAAGCTGGTAA CAGAGACCACATTA 720
Db 85469 TGTGTGAATCCTTTTTCCTGCTATCCAGCAGATGAGAAGCTGGTAA CAGAGACCACATTA 85528
Qy 721 GTTGGAGACTAAAGATCATTTGACATTTCACTGCTGAGTTGTATTTGAGTAATTTTA 780
Db 85529 GTTGGAGACTAAAGATCATTTGACATTTCACTGCTGAGTTGTATTTGAGTAATTTTA 85588
Qy 781 GTTGAACCTCAC-TTTGTAAATCTTGACA CAGGGGCAATCCAAATCTGCACAAGAGATAT 839
Db 85589 GTTGAACCTCACTTTTGTAAATCTTGACA CAGGGG-- -CATCCATATCTGCAC-AGAGATAT 85644
Qy 840 GTTAAACA GTGTAAATGCTGCATGAGAGATTGGGTGATTTTACTTTCGTTTGTGC 899
Db 85645 GTTAA-CA GTGTAAATGCTGCATGAGAGATTGGGTGATTTTACTTTCGTTTGTGC 85703
Qy 900 TCTTCTTCTTATTTGTTCTTACTTATTTACGATTACCCCTATCGTTTCCAAATGTAAA 959
Db 85704 TCTTCTTCTTATTTGTTCTTACTTATTTACGATTACCCCTATCGTTT-CCAAATGTAAA 85762
Qy 960 AGGCCATTTTGAAGCCTAATTCAACCTTCACTATTTTGTATCTAAGTATTCACCTT 1019
Db 85763 AGGCCATTTTGAAGCCTAATTCAACCTTCACTATTTTGTATCTAAGTATTCACCTT 85822
Qy 1020 GATTGAGACTGGGTAGACAGGTGAAACCATATCAAGGTTTAAATTTTAAATTTTAA 1079
Db 85823 GATTGAGACTGGGTAGACAGGTGAAACCATATCAAGGTTTAAATTTTAAATTTTAA 85882
Qy 1080 TATTATTTATTTATTTATTTTGAATGAGTGTGGCTGTGCCCCAGGCTGAGTGA 1139
Db 85883 TATTATTTATTTATTTATTTTGAATGAGTGTGGCTGTGCCCCAGGCTGAGTGA 85942
Qy 1140 GCGGCGTATCA CAGTTCATG CAGCCTCAACCTTCTAGGCTCAAGGATTTCTCCACCT 1199
Db 85943 GCGGCGTATCA CAGTTCATG CAGCCTCAACCTTCTAGGCTCAAGGATTTCTCCACCT 86002
Qy 1200 CAGCCCCCAAGTAGTTGGGACCA CAGTATGCGCCACCATGCTGGCTAATTTCTTAT 1259
Db 86003 CAGCCCCCAAGTAGTTGGGACCA CAGTATGCGCCACCATGCTGGCTAATTTCTTAT 86062
Qy 1260 TTTTGTGAGAGATAGGATCTCACTATATTTGTCCAGGCTGGTGTGAATTTCTGGGCTAG 1319
Db 86063 TTTTGTGAGAGATAGGATCTCACTATATTTGTCCAGGCTGGTGTGAATTTCTGGGCTAG 86122
Qy 1320 GTGAGCCTCCCA CCTGGGCTCCCAAAGTACTGGATTACAGGCATGAGCCAAAGGTCCCC 1379
Db 86123 GTGAGCCTCCCA CCTGGGCTCCCAAAGTACTGGATTACAGGCATGAGCCAAAGGTCCCC 86182
Qy 1380 TGCCCATATGAGATTTTCTGTCTGTGATCCCATG CAGCTAGTAATCAAGACTTGCTGC 1439
Db 86183 TGCCCATATGAGATTTTCTGTCTGTGATCCCATG CAGCTAGTAATCAAGACTTGCTGC 86242
Qy 1440 TGACTCTGAGAGACTGCATGCTTCTTGAGCTGTGAACCTTCAAGCTTAAAGCTCATAG 1499
Db 86243 TGACTCTGAGAGACTGCATGCTTCTTGAGCTGTGAACCTTCAAGCTTAAAGCTCATAG 86302
Qy 1500 GCAGCCCTGA AACCCCAAAGGTTCTATGCTTTATCATCTCGATCATGTTGATTTT 1559
Db 86303 GCAGCCCTGA AACCCCAAAGGTTCTATGCTTTATCATCTCGATCATGTTGATTTT 86362
Qy 1560 ATAGAATAAACA CATGAATTAAAGACTA CCGCTCAAAGCTGAGCAAACTTAAATTTT 1619

Db 86363 ATAGAATAAACA CATGAATTAAAGACTA CCGCTCAAAGCTGAGCAAACTTAAAGCTATTT 86422
Qy 1620 TTTTAAAGTTGACCTGTTTAAATCACTCTTGAGAAAAAGAAAAATTAATACAAATA 1679
Db 86423 TTTTAAAGTTGACCTGTTTAAATCACTCTTGAGAAAAAGAAAAATTAATACAAATA 86482
Qy 1680 ATTAACGGTGAATACAGGCTACTATACTTGTGTTCTCCAGAAATTAAGCAGTCTGTCTTT 1739
Db 86483 ATTAACGGTGAATACAGGCTACTATACTTGTGTTCTCCAGAAATTAAGCAGTCTGTCTTT 86542
Qy 1740 TCTTGCTTTAGATGCTGAAGTGAGAAAGGACACTCTGTGATTTGATGTTGTACTGACA 1799
Db 86543 TCTTGCTTTAGATGCTGAAGTGAGAAAGGACACTCTGTGATTTGATGTTGTACTGACA 86602
Qy 1800 AAATGTATTTTTTTCTCAGCTGCTATGATTTGATTTATGATTAAGATG 1859
Db 86603 AAATGTATTTTTTTCTCAGCTGCTATGATTTGATTTATGATTAAGATG 86662
Qy 1860 CTGATGGAGCACACAAACCATTTGTTCTCAGTCCATTTTCTCCTCAAAAGCCTGG 1919
Db 86663 CTGATGGAGCACACAAACCATTTGTTCTCAGTCCATTTTCTCCTCAAAAGCCTGG 86722
Qy 1920 AATGTCCATTTGATCAGTGGAGATGTACCTGACAGACCCATGAAAAAGATCAACAA 1979
Db 86723 AATGTCCATTTGATCAGTGGAGATGTACCTGACAGACCCATGAAAAAGATCAACAA 86782
Qy 1980 TTCCACCAAGGAGCCCTATTTTCTTAATTTCAATTGAAATGCTCTAATGTCTTC 2039
Db 86783 TTCCACCAAGGAGCCCTATTTTCTTAATTTCAATTGAAATGCTCTAATGTCTTC 86842
Qy 2040 TTTCAATCTGCTTCTCTACCAAGTTTACAGCTTTTCTGTGTTCAAAATGTACTCAT 2099
Db 86843 TTTCAATCTGCTTCTCTACCAAGTTTACAGCTTTTCTGTGTTCAAAATGTACTCAT 86902
Qy 2100 ACACTCTCATTTTCTCTCATCACAA CCCCAGTGACCCCAATGCTCTCATTTGATATA 2159
Db 86903 ACACTCTCATTTTCTCTCATCACAA CCCCAGTGACCCCAATGCTCTCATTTGATATA 86962
Qy 2160 AGTAAAGAGGCTCTGCATTTAAGGCTGTGCCAAGG CAGCAGTGAAGGCGCTAGGAC 2219
Db 86963 AGTAAAGAGGCTCTGCATTTAAGGCTGTGCCAAGG CAGCAGTGAAGGCGCTAGGAC 87022
Qy 2220 TGGCTCCATTTCCATCTTATTTCACTGACTTTGACTACCCAGAACCCCAATGTGG 2279
Db 87023 TGGCTCCATTTCCATCTTATTTCACTGACTTTGACTACCCAGAACCCCAATGTGG 87082
Qy 2280 GCGTCAGTATTCGATCAATTAATTTAATTAAGAACAAAACAATTTCCCGCATTTGCCCC 2339
Db 87083 GCGTCAGTATTCGATCAATTAATTTAATTAAGAACAAAACAATTTCCCGCATTTGCCCC 87142
Qy 2340 AGTTATTAAGCATTTCTCAGATTTTACCTTGAAGAAATGCCATGCGCTGTATTTACAT 2399
Db 87143 AGTTATTAAGCATTTCTCAGATTTTACCTTGAAGAAATGCCATGCGCTGTATTTACAT 87202
Qy 2400 CTTGACCTTGTCCTTCTCTCCTAGAAAGGAGAAAGTCA GTTGAAGCCCTCTGAGGAAC 2459
Db 87203 CTTGACCTTGTCCTTCTCTCCTAGAAAGGAGAAAGTCA GTTGAAGCCCTCTGAGGAAC 87262
Qy 2460 TAGTGAATGCTTAATCTGTCTTCATGACTTCCTGCTTATCTGTTTCTATTTTCTCC 2519
Db 87263 TAGTGAATGCTTAATCTGTCTTCATGACTTCCTGCTTATCTGTTTCTATTTTCTCC 87322
Qy 2520 TTTTCCACCGAAGTCTATTAATCTCAAGAAAGCAGGCA CTGGCTTAAGGCTCTGGCCT 2579
Db 87323 TTTTCCACCGAAGTCTATTAATCTCAAGAAAGCAGGCA CTGGCTTAAGGCTCTGGCCT 87382
Qy 2580 AAGAAATATCAAGTCCAGTGAGAAATCCCAATTGA CTGACCCCTCTGCTTAACCCCTTGT 2639
Db 87383 AAGAAATATCAAGTCCAGTGAGAAATCCCAATTGA CTGACCCCTCTGCTTAACCCCTTGT 87442
Qy 2640 GATGGAAGGCTCCAGGGGTTGCTTTTGTGATGTTACAGGCTTA ACTCAGCATCAC 2699
Db 87443 GATGGAAGGCTCCAGGGGTTGCTTTTGTGATGTTACAGGCTTA ACTCAGCATCAC 87502

QY	2700	AGGGCAAGAAAGAAAGTAACCTAACTAATGCTGCTTAAATTGTAATTATTTGTAAT	2759
Db	87503	AGGGCAAGAAAGAAAGTAACCTAACTAATGCTGCTTAAATTGTAATTATTTGTAAT	87562
QY	2760	AGTTAATTACTGTGATTGTACATGTGTAAACAGACAAAAATGTGTATTTTTTTCACAGCTGC	2819
Db	87563	AGTTAATTACTGTGATTGTACATGTGTAAACAGACAAAAATGTGTATTTTTTTCACAGCTGC	87622
QY	2820	TGTGATTGGATTATGCCCATTGGAAATAAGAATGCTGTTAAGACACACAGCCAGGTTTC	2879
Db	87623	TGTGATTGGATTATGCCCATTGGAAATAAGAATGCTGTTAAGACACACAGCCAGGTTTC	87682
QY	2880	CTCAAGTCCGTAGCAAAATTTTCAAAAAGTTAAATTAAATCACTACATTGGAATCTAG	2939
Db	87683	CTCAAGTCCGTAGCAAAATTTTCAAAAAGTTAAATTAAATCACTACATTGGAATCTAG	87742
QY	2940	TGACAGAGAAATGACATGAGTAGAGACTAAAGATCTAGCCCAATTTATATTACTT	2999
Db	87743	TGACAGAGAAATGACATGAGTAGAGACTAAAGATCTAGCCCAATTTATATTACTT	87802
QY	3000	GTTAGAGATTTTGAACAAATTACTAAATTTCTTCAAGGTTCAATTTCCCATTAACAT	3059
Db	87803	GTTAGAGATTTTGAACAAATTACTAAATTTCTTCAAGGTTCAATTTCCCATTAACAT	87862
QY	3060	AATGAATGTCATCATATTATGGGGCCGTGAGAGACATAATTACTTGTAAATTGTAATAAT	3119
Db	87863	AATGAATGGCTCATCATATTATGGGGCCGTGAGAGACATAATTACTTGTAAATTGTAATAAT	87922
QY	3120	CATTGTTATTATTATTATACATATTTGCTTTTAAATGAGATAAGATTTTAAAGGTATAT	3179
Db	87923	CATTGTTATTATTATTATACATATTTGCTTTTAAATGAGATAAGATTTTAAAGGTATAT	87982
QY	3180	GTAACCTGTAAAAACATAAAATGCAAAATGCCGTAGAGACAGTAGTAATAATAATGATTA	3239
Db	87983	GTAACCTGTAAAAACATAAAATGCAAAATGCCGTAGAGACAGTAGTAATAATAATGATTA	88042
QY	3240	TTAATTTGTATCATATATAGCCGTTTTTTTCTGTTGTGTAATTTCTTCTTTAAATGC	3299
Db	88043	TTAATTTGTATCATATATAGCCGTTTTTTTCTGTTGTGTAATTTCTTCTTTAAATGC	88102
QY	3300	TTACAGAAATCTGTATCCCATTTCTCAACCAACCCCAACAACATTTCTGCTTCTTTCC	3359
Db	88103	TTTACAGAAATCTGTATCCCATTTCTCAACCAACCCCAACAACATTTCTGCTTCTTTCC	88162
QY	3360	CATGCC-GGTCATGCTAATCTTGAAGCTTCAGCTCTTCCCTTCATCCTCTCTCCCTG	3418
Db	88163	CATGCCGGGTCATGCTAATCTTGAAGCTTCAGCTCTTCCCTTCATCCTCTTCTCTG	88222
QY	3419	GCACCTCTGATATGCCCTTTGAAATTCATGTTAAAGAATCCCTAGGCTGCTATCACATGT	3478
Db	88223	GCACCTCTGATATGCCCTTTGAAATTCATGTTAAAGAATCCCTAGGCTGCTATCACATGT	88282
QY	3479	GGCATCTTGTGTAGTACATGAATAATCACTGTGTGTTTACGAAGATGATTATGC	3538
Db	88283	GGCATCTTGTGTAGTACATGAATAATCACTGTGTGTTTACGAAGATGATTATGC	88342
QY	3539	TTCAATTGTGGATTGTATTTTCTTCTTCATACACAGGAGAGATGAA	3586
Db	88343	TTCAATTGTGGATTGTATTTTCTTCTTCATACACAGGAGAGATGAA	88390

RESULT 7
AC104439 197279 bp DNA linear PRI 20-JUN-2002
LOCUS AC104439 Homo sapiens chromosome 3 clone RP11-793B15, complete sequence.
DEFINITION AC104439 AC024739
ACCESSION AC104439.2 GI:21490240
VERSION AC104439.2
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

REFERENCE	Hominidae; Homo.
AUTHORS	1 (bases 1 to 197279) Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z., Saenphimmachak,C., Phelps,K.A., Buckley,D., Kibukawa,M., Raymond,C. and Haugen,E.D.
TITLE	Unpublished
JOURNAL	2 (bases 1 to 197279)
AUTHORS	Kaul,R.K., Olson,M.V., Raymond,C. and Haugen,E.D.
TITLE	Direct Submission
JOURNAL	Submitted (11-DEC-2001) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA
REFERENCE	3 (bases 1 to 197279) Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z., Saenphimmachak,C., Phelps,K.A., Buckley,D., Kibukawa,M., Raymond,C. and Haugen,E.D.
AUTHORS	Direct Submission
TITLE	Submitted (20-JUN-2002) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA
JOURNAL	On Jun 20, 2002 this sequence version replaced gi:17488621.
COMMENT	Genome Center

Center: University of Washington Genome Center
Center Code: UWGC
Web site: http://www.genome.washington.edu
Contact: uwgchtgs@u.washington.edu
Drafting Center: WUGSC
----- Project Information
Center project name: chr-3
Center clone name: RP11-793B15 (bc0564)
----- Summary Statistics
Sequencing vector: unknown; 52% of reads
Sequencing vector: plasmid; 108752; 48% of reads
Chemistry: Dye-terminator BT; 94% of reads
Chemistry: Dye-terminator Big Dye; 6% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 197168 bases at least Q40
Consensus quality: 197255 bases at least Q30
Consensus quality: 197275 bases at least Q20
Insert size: 197279; sum-of-contigs
Quality coverage: 8.2x in Q20 bases; sum-of-contigs

Overlapping Sequences:
5': RP11-91E8 (UWGC:bc0216) AC026349
3': CTD-2563A18 (UWGC:bc0730)

Sequence Quality Assessment:
This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp. Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

Sequence Validation:
This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered

fragments are separated by dashed lines.

HindIII		BglII		EcoRI	
SeqDerMap	FngPrnt	SeqDerMap	FngPrnt	SeqDerMap	FngPrnt
-----	-----	-----	-----	-----	-----
2687	2617	8949	8586	8696	8661
-----	-----	-----	-----	-----	-----
6382	6410	2067	2160	6	<800
-----	-----	-----	-----	-----	-----
512	<800	7846	7940	2742	2803
-----	-----	-----	-----	-----	-----
449	<800	3734	3895	5376	5324
-----	-----	-----	-----	-----	-----
2602	2763	1334	1301	1493	1478
-----	-----	-----	-----	-----	-----
2590	2617	2287	2309	823	835
-----	-----	-----	-----	-----	-----
8313	8291	1814	1918	1962	2002
-----	-----	-----	-----	-----	-----
1711	1683	691	<800	2900	2954
-----	-----	-----	-----	-----	-----
9821	9472	5477	5348	1484	1478
-----	-----	-----	-----	-----	-----
516	<800	305	<800	1005	995
-----	-----	-----	-----	-----	-----
8587	8291	25245	25541	1181	1171
-----	-----	-----	-----	-----	-----
7446	7581	3988	4121	18560	19002
-----	-----	-----	-----	-----	-----
2088	2075	1633	1598	3603	3579
-----	-----	-----	-----	-----	-----
2509	2617	631	<800	4943	5076
-----	-----	-----	-----	-----	-----
3519	3501	90	<800	3239	3241
-----	-----	-----	-----	-----	-----
26	<800	402	<800	953	995
-----	-----	-----	-----	-----	-----
925	933	3350	3490	1621	1615
-----	-----	-----	-----	-----	-----
98	<800	4577	4515	6827	6900
-----	-----	-----	-----	-----	-----
6409	6410	1229	1183	79	<800
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1383	1376	4221	4331	16418	16263
-----	-----	-----	-----	-----	-----
16048	15829	3980	4121	3361	3241
-----	-----	-----	-----	-----	-----
1876	1877	2548	2497	872	881
-----	-----	-----	-----	-----	-----
4169	4068	674	<800	4220	4193
-----	-----	-----	-----	-----	-----
1674	1683	2332	2309	2848	2803
-----	-----	-----	-----	-----	-----
52	<800	11445	11045	2283	2318
-----	-----	-----	-----	-----	-----
5227	5082	5692	5632	3211	3241
-----	-----	-----	-----	-----	-----
15464	15829	1385	1414	4615	4632
-----	-----	-----	-----	-----	-----
14333	14296	608	<800	6823	6900
-----	-----	-----	-----	-----	-----
1026	1026	3930	3895	886	881
-----	-----	-----	-----	-----	-----
645	<800	1465	1414	2032	2002
-----	-----	-----	-----	-----	-----
6621	6410	2382	2497	8680	8661
-----	-----	-----	-----	-----	-----
8413	8291	747	<800	5163	5076
-----	-----	-----	-----	-----	-----
1401	1376	1951	2012	1547	1478
-----	-----	-----	-----	-----	-----

	1512	1471	642	<800	7058	6900
-----	-----	-----	-----	-----	-----	-----
	5801	5644	21060	21003	1647	1615
-----	-----	-----	-----	-----	-----	-----
	3256	3278	3700	3666	2753	2803
-----	-----	-----	-----	-----	-----	-----
	3448	3501	1321	1301	162	<800
-----	-----	-----	-----	-----	-----	-----
	2738	2763	10705	10502	1078	1093
-----	-----	-----	-----	-----	-----	-----
	237	<800	3128	3317	2156	2173
-----	-----	-----	-----	-----	-----	-----
	6715	6823	183	<800	5077	5076
-----	-----	-----	-----	-----	-----	-----
	201	<800	3255	3490	154	<800
-----	-----	-----	-----	-----	-----	-----
	1002	1026	5693	5632	1571	1478
-----	-----	-----	-----	-----	-----	-----
	221	<800	3380	3317	219	<800
-----	-----	-----	-----	-----	-----	-----
	2854	2899	237	<800	520	<800
-----	-----	-----	-----	-----	-----	-----
	6998	7317	431	<800	1540	1478
-----	-----	-----	-----	-----	-----	-----
	1174	1145	2152	2160	1479	1478
-----	-----	-----	-----	-----	-----	-----
	7876	8291	249	<800	1613	1615
-----	-----	-----	-----	-----	-----	-----
	1911	1877	2599	2778	1399	1478
-----	-----	-----	-----	-----	-----	-----
	3899	3847	685	<800	9553	9383
-----	-----	-----	-----	-----	-----	-----
	5672	5644	41	<800	166	<800
-----	-----	-----	-----	-----	-----	-----
	1711	1683	388	<800	13615	13115
-----	-----	-----	-----	-----	-----	-----
	862	854	2500	2497	4731	4632
-----	-----	-----	-----	-----	-----	-----
	2368	2389	2889	2778	5159	5076
-----	-----	-----	-----	-----	-----	-----
			178	<800	4503	4430
-----	-----	-----	-----	-----	-----	-----
			6589	6728	6607	6900
-----	-----	-----	-----	-----	-----	-----
			3836	3895	2766	2803
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Query Match

Best Local Similarity 97.4%; Score 3493.8; DB 8; Length 197279;

Matches 3568; Conservativity 0; Mismatches 12; Indels 8; Gaps 6;

Qy	1	GGATCCCTACCTTCCCATCAGAGCTAGGCGGCATGAGCGCTCTCTGCTAAGATGGGA	60
Db	186606	GGATCCCTACCTTCCCATCAGAGCTAGGCGGCATGAGCGCTCTCTGCTAAGATGGGA	186665
Qy	61	CCCCAAGGATGTCTCCCTGTGGGCACTTCTTACCAAGATGGATGGCCAGTCCGTT	120
Db	186666	CCCCAAGGATGTCTCCCTGTGGGCACTTCTTACCAAGATGGATGGCCAGTCCGTT	186725
Qy	121	AAGTGTGTGTGAGGAGAAAAAAGATCTAGTTGTACTCTTGAGAGTTCCTCGTTT	180
Db	186726	AAGTGTGTGTGAGGAGAAAAAAGATCTAGTTGTACTCTTGAGAGTTCCTCGTTT	186785
Qy	181	GTTCAATGCATGGGAGGAGTCAAGAGGAGCAGAGCCTTGCTCAGTGCTTACAGTGCA	240
Db	186786	GTTCAATGCATGGGAGGAGTCAAGAGGAGCAGAGCCTTGCTCAGTGCTTACAGTGCA	186845
Qy	241	GGAAGAGTGTCATAGCCTGGGCCAGGGCCAGGCCCTGTGTGAGGCGGTAGTGTAACAGA	300
Db	186846	GGAAGAGTGTCATAGCCTGGGCCAGGGCCAGGCCCTGTGTGAGGCGGTAGTGTAACAGA	186905
Qy	301	GAGGCTCTCCATTCCAGGCCCAAGAGACTAAGATGAATACCTCATGATATTAGC	360
Db	186906	GAGGCTCTCCATTCCAGGCCCAAGAGACTAAGATGAATACCTCATGATATTAGC	186965

QY 361 TACAACACACACAGAGGTTCCAGAAAAAGGCTCAGCGTTGGAAACGAGTCACCCCCAC 420
 DB 186966 TACAACACACACAGAGGTTCCAGAAAAAGGCTCAGCGTTGGAAACGAGTCACCCCCAC 187025
 QY 421 TCAGCAGACACACAGTCATATAATCAAGAACCAACAGAGACAGGAACACCCCTTCCCA 480
 DB 187026 TCAGCAGACACACAGTCATATAATCAAGAACCAACAGAGACAGGAACACCCCTTCCCA 187085
 QY 481 CTCTGCCCCCATGTCCTCAAGTTGTAGTGGCCCTTCTCCAGATCTCTGCCACCATCTTGA 540
 DB 187086 CTCTGCCCCCATGTCCTCAAGTTGTAGTGGCCCTTCTCCAGATCTCTGCCACCATCTTGA 187145
 QY 541 AAGGAACA CTGAAAGAAGAACTGAAATTATAGCTGACAGCATAAAGAGATGAGTAAA 600
 DB 187146 AAGGAACA CTGAAAGAAGAACTGAAATTATAGCTGACAGCATAAAGAGATGAGTAAA 187205
 QY 601 ACCTAAATCATTTGTTCAACATGAATGAATCAAGAGAATTAAACCACTTGGACTAAA 660
 DB 187206 ACCTAAATCATTTGTTCAACATGAATGAATCAAGAGAATTAAACCACTTGGACTAAA 187265
 QY 661 TGTGTGAATCCTTTTCTCTGCTATCCAGACAGATGAGAAGCTGTAAACAGAACCAATA 720
 DB 187266 TGTGTGAATCCTTTTCTCTGCTATCCAGACAGATGAGAAGCTGTAAACAGAACCAATA 187325
 QY 721 GTTTGAGACTTAAAGATCATTTGACATTTCACTGCTGAGTTGTATTTGAGTAATTTTA 780
 DB 187326 GTTTGAGACTTAAAGATCATTTGACATTTCACTGCTGAGTTGTATTTGAGTAATTTTA 187385
 QY 781 GTTGACCTCAC-TTTGTAAATCTTGACACAGGGGCAATCCAATATCTGCAACAAGATAT 839
 DB 187386 GTTGACCTCAC-TTTGTAAATCTTGACACAGGGG--CATCCATATCTGCAAC-AGAGATAT 187441
 QY 840 GTTAAACAGTGTAAATGCTGCATGAGAGATTGGGTGATTTTACTTTCGTTTGTGC 899
 DB 187442 GTTAA-CAGTGTAAATGCTGCATGAGAGATTGGGTGATTTTACTTTCGTTTGTGC 187500
 QY 900 TCTTCTTCTTATTTGTTCTTACTTATTTACGATTAACCTATCGTTTCCCAAATGTAAA 959
 DB 187501 TCTTCTTCTTATTTGTTCTTACTTATTTACGATTAACCTATCGTTT-CCAAATGTAAA 187559
 QY 960 AGGCCATTTTGAAGCCTAATTCAAACTCTTCACTATTTTGTATCTAAGTATTCACCT 1019
 DB 187560 AGGCCATTTTGAAGCCTAATTCAAACTCTTCACTATTTTGTATCTAAGTATTCACCT 187619
 QY 1020 GATTGAGCTGGGTAGACAGGTGAAAAACATATCAGGTTTAAATTTTAAATTTTAAAT 1079
 DB 187620 GATTGAGCTGGGTAGACAGGTGAAAAACATATCAGGTTTAAATTTTAAATTTTAAAT 187679
 QY 1080 TATTTATTTATTTATTTATTTTGTAGATGAGTCTGGCTGTGCCCCAGGCTGAGTGCA 1139
 DB 187680 TATTTATTTATTTATTTATTTTGTAGATGAGTCTGGCTGTGCCCCAGGCTGAGTGCA 187739
 QY 1140 GCGGCGTATCACAGTTCACGTGAGCCTCAACTTCTAGGCTCAAGGATTTCTCCACCT 1199
 DB 187740 GCGGCGTATCACAGTTCACGTGAGCCTCAACTTCTAGGCTCAAGGATTTCTCCACCT 187799
 QY 1200 CAGCCCCCAAGTAGTTGGACCAACGTATGCCCAACCATGCGCTGCTAATTTCTTAT 1259
 DB 187800 CAGCCCCCAAGTAGTTGGACCAACGTATGCCCAACCATGCGCTGCTAATTTCTTAT 187859
 QY 1260 TTTTGTAGAGATAGGATCTCACTATATTTGTCCAGGCTGTGTGTAATTTCTGGGCTCAG 1319
 DB 187860 TTTTGTAGAGATAGGATCTCACTATATTTGTCCAGGCTGTGTGTAATTTCTGGGCTCAG 187919
 QY 1320 GTGAGCCTTCCACCTGGGCTCCCAAAGTACTGGGATTAACAGGCATGAGCCAAAGTCCCC 1379
 DB 187920 GTGAGCCTTCCACCTGGGCTCCCAAAGTACTGGGATTAACAGGCATGAGCCAAAGTCCCC 187979
 QY 1380 TGCCCATATGAGATTTTCTGTCTGTATCCCATGACGCTAGTAATCAAGGACTTGGCTGC 1439
 DB 187980 TGCCCATATGAGATTTTCTGTCTGTATCCCATGACGCTAGTAATCAAGGACTTGGCTGC 188039

QY 1440 TGACTCTGAGGACCTGCATGCTTTCTTGAGCTGTGAACCTTCAGTGCTAAAAAGCTCATAG 1499
 DB 188040 TGACTCTGAGGACCTGCATGCTTTCTTGAGCTGTGAACCTTCAGTGCTAAAAAGCTCATAG 188099
 QY 1500 GCAGCCCTGAAACCCAAACCAAAGGTTCTATGTGTTATCATCTGATCATGTGATTTT 1559
 DB 188100 GCAGCCCTGAAACCCAAACCAAAGGTTCTATGTGTTATCATCTGATCATGTGATTTT 188159
 QY 1560 ATAGAATTAACACATGAATTAAGAACACTACCTCAACCTGAGCAAAACTTAAGTAATTT 1619
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 QY 1620 TTTTAAAGTTGACCTGTTTTAAATCACTCTTGAGAAAAAGAAAAATTAATACAAATA 1679
 DB 188220 TTTTAAAGTTGACCTGTTTTAAATCACTCTTGAGAAAAAGAAAAATTAATACAAATA 188279
 QY 1680 ATTAAAGGTGAATACAGGCTACTATACCTTTGTTCTCCGAATTAAGAGTTCTGTCTTT 1739
 DB 188280 ATTAAAGGTGAATACAGGCTACTATACCTTTGTTCTCCGAATTAAGAGTTCTGTCTTT 188339
 QY 1740 TCTTCTTTAGATGCTGAAGTGAAGAAGACACTCTGTGATTTGACGTGTGAACGTACA 1799
 DB 188340 TCTTCTTTAGATGCTGAAGTGAAGAAGACACTCTGTGATTTGACGTGTGAACGTACA 188399
 QY 1800 AAATGTATTTTTTTTCTCACGCTGCTATGATTTGGAATATGCTATTATGAATAAGATG 1859
 DB 188400 AAATGTATTTTTTTTCTCACGCTGCTATGATTTGGAATATGCTATTATGAATAAGATG 188459
 QY 1860 CTGATGGGAGCACACAAACCAATTTGTTCTCTCAGTCCATTTTCTCCTCAAAAGCCTGG 1919
 DB 188460 CTGATGGGAGCACACAAACCAATTTGTTCTCTCAGTCCATTTTCTCCTCAAAAGCCTGG 188519
 QY 1920 AATGTGCCATTGATCAGTGGAGATGTACCTTGACACAGCCCATGAAAAAGATCAACAA 1979
 DB 188520 AATGTGCCATTGATCAGTGGAGATGTACCTTGACACAGCCCATGAAAAAGATCAACAA 188579
 QY 1980 TTCCACCCAAAGGACCCCTATTTTCTCTAATTTTCAATTTGAAATGGCTTCTAATGTCTTC 2039
 DB 188580 TTCCACCCAAAGGACCCCTATTTTCTCTAATTTTCAATTTGAAATGGCTTCTAATGTCTTC 188639
 QY 2040 TTTCAATTCCTGCTTCTCTCAACAGTTTAAACAGTTTCTGTGTTCAAAATGTAACCTCACAT 2099
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 QY 2100 ACACTCTCATTTTCTCTCATCACAAACCCCAAGTGACCCCAATGCTCTCATCTTGCATATA 2159
 DB 188700 ACACTCTCATTTTCTCTCATCACAAACCCCAAGTGACCCCAATGCTCTCATCTTGCATATA 188759
 QY 2160 AGTAAAGAGGCTCTGCATTAAGGCTGTGTCAAAGCACGCACTGAGAGCGCTAGAC 2219
 DB 188760 AGTAAAGAGGCTCTGCATTAAGGCTGTGTCAAAGCACGCACTGAGAGCGCTAGAC 188819
 QY 2220 TGGCTGCATTTCCATCTCTATTTCTCACTGAATTTGACTAACCCCAACATGTGG 2279
 DB 188820 TGGCTGCATTTCCATCTCTATTTCTCACTGAATTTGACTAACCCCAACATGTGG 188879
 QY 2280 GCGTCAATTTGATCAATTAATTTTAAGAAGCAAAACAATTTCCCGCATTTGCCCC 2339
 DB 188880 GCGTCAATTTGATCAATTAATTTTAAGAAGCAAAACAATTTCCCGCATTTGCCCC 188939
 QY 2340 AGTTATTAAGCATTTCTCAGATTTACCTTGAGAAATGCCATGGCCTGTATATTCACAT 2399
 DB 188940 AGTTATTAAGCATTTCTCAGATTTACCTTGAGAAATGCCATGGCCTGTATATTCACAT 188999
 QY 2400 CTTACACCTTGTCCCTTCTCTAGAAAAGAGAAAGTCAAGTTGATGCCCTTGAGGAAC 2459
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 QY 2520 TTTTCCACGGAAGTCTATATCTCAAGAAAAAGCAGGCACTGGCCTTAGGGCTCCTGCGCT 2579

Db	189120	TTTTCCACCGAAGTCTATAATCTCAAGAAAAGCAGGACTGGCCTTAGGGCTCCTGGCCT	1891179
Qy	2580	AAGAAATATCAAGTCCAGTGAAGAAATCCCATTTGACTGAACCCCTCCTGCTTAAACCCCTTGT	2639
Db	189180	AAGAATATCAAGTCCAGTGAAGAAATCCCATTTGACTGAACCCCTCCTGCTTAAACCCCTTGT	1892339
Qy	2640	GATGGAAGACTCCAGGGGTTTGCTTTTGGCATGTAAACAGGCCCTAACTCAGCATCACC	2699
Db	189240	GATGGAAGACTCCAGGGGTTTGCTTTTGGCATGTAAACAGGCCCTAACTCAGCATCACC	1892999
Qy	2700	AGGGGCAAGAAAAGAAAGTAACTTAACTAATGCTGCTTATTAATTGTAATTATTGTAAT	2759
Db	189300	AGGGGCAAGAAAAGAAAGTAACTTAACTAATGCTGCTTATTAATTGTAATTATTGTAAT	1893599
Qy	2760	AGTTAATTACTGTGATTGTACATGTGTACACAGCAAAATGTGATTTTTTTCACAGCTGC	2819
Db	189360	AGTTAATTACTGTGATTGTACATGTGTACACAGCAAAATGTGATTTTTTTCACAGCTGC	1894199
Qy	2820	TGTGATTGGATTATGCCATTGGGAATAGAATGCTGTTAAGAGCACAGCCAGGTTTC	2879
Db	189420	TGTGATTGGATTATGCCATTGGGAATAGAATGCTGTTAAGAGCACAGCCAGGTTTC	1894799
Qy	2880	CTCAAGTCCGTAGCAAAATTTTCAAAAAGTTAAATTTAAAAATCACTACATTTGAATCTAG	2939
Db	189480	CTCAAGTCCGTAGCAAAATTTTCAAAAAGTTAAATTTAAAAATCACTACATTTGAATCTAG	1895399
Qy	2940	TGACAGAGAAATGACATGGATAGAGACTAAAGACTAAGCCCAAATTTATATTACTT	2999
Db	189540	TGACAGAGAAATGACATGGATAGAGACTAAAGACTAAGCCCAAATTTATATTACTT	1895999
Qy	3000	GTTAGAGGATTTTGAACAAATTACTAAATTTCTTCAAGTTCAATTTCCCAATTAACTAT	3059
Db	189600	GTTAGAGGATTTTGAACAAATTACTAAATTTCTTCAAGTTCAATTTCCCAATTAACTAT	1896599
Qy	3060	AATGAATGCTCATCATTAATGGGGCCCTGAGAGAGCATTAATTAATTGTAATTAAT	3119
Db	189660	AATGAATGCTCATCATTAATGGGGCCCTGAGAGAGCATTAATTAATTGTAATTAAT	1897199
Qy	3120	CATTGTTATTATTATTATACATATTTTGCTTTTAAATGATTAAGGATTTTAAAGTATAT	3179
Db	189720	CATTGTTATTATTATTATACATATTTTGCTTTTAAATGATTAAGGATTTTAAAGTATAT	1897799
Qy	3180	GTAACCTGTAAACATATAAAATGCAAAATGCCGTAAAGACAGTAGTAATAATAGATTAA	3239
Db	189780	GTAACCTGTAAACATATAAAATGCAAAATGCCGTAAAGACAGTAGTAATAATAGATTAA	1898399
Qy	3240	TTATATGTTATCATTTATCTAGCGCTGTTTTTTCCTGTTGTGATTTCTTCCCTTAAATGC	3299
Db	189840	TTATATGTTATCATTTATCTAGCGCTGTTTTTTCCTGTTGTGATTTCTTCCCTTAAATGC	1898999
Qy	3300	TTTACAGAAATCTGTATCCCAATCTTACACCAACCCCAACAATTTGCTTCTTTTCC	3359
Db	189900	TTTACAGAAATCTGTATCCCAATCTTACACCAACCCCAACAATTTGCTTCTTTTCC	1899599
Qy	3360	CATGCC-GGTTCATGCTAACTTTGAAAAGCTTCAGCTCTTTCCTTCCGAATCCTTCTCCTG	3418
Db	189960	CATGCCGGGTTCATGCTAACTTTGAAAAGCTTCAGCTCTTTCCTTCCGAATCCTTCTCCTG	1900199
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SEQUENCING IN PROGRESS ***	26 ordered pieces.				
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VERSION	AJ312688.2	GI:13559235			
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ORGANISM	Homo sapiens				
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REFERENCE	1				
AUTHORS	Kiss,H., Yang,Y., Kiss,C., Andersson,K., Klein,G., Imreh,S. and Dumanski,J.P.				
TITLE	The transcriptional map of the common eliminated region 1 (C3CER1) in 3p21.3				
JOURNAL	Eur. J. Hum. Genet. 10 (1), 52-61 (2002)				
PUBMED	11896456				
REFERENCE	2 (bases 1 to 220965)				
AUTHORS	Kiss,H.				
TITLE	Direct Submission				
JOURNAL	Submitted (01-APR-2001) Kiss H.; Microbiology and Tumorbiology Center (MTC), Karolinska Institute, Box 280, Stockholm, S-17177, SWEDEN				
COMMENT	On Apr 5, 2001 this sequence version replaced gi:13548633. The sequence is a consensus sequence of clone RP4-787c23 (1-140400 bp), clone RP6-32g23 (31212-220965 bp), clone RP6-146e1 (partially, 1-6800 bp) and clone RP6-188g11 (partially, 1-108303 bp). The sequencing contigs are in order and the gaps between them are represented by 100 Ns.				
	Contig 1:				
	1-11731 bp	Contig 2: 11832-26218 bp	Contig 3: 26319-28347 bp		
	Contig 4:				
	28448-42160 bp	Contig 5: 42261-55059 bp	Contig 6: 55160-61578 bp		
	Contig				
	7: 61679-97342 bp	Contig 8: 97443-117655 bp	Contig 9:		
	117756-118727 bp				
	Contig 10: 118828-121834 bp	Contig 11: 121935-127855 bp	Contig		
	12:				
	127956-129383 bp	Contig 13: 129484-131747 bp	Contig 14:		
	131848-132316 bp				
	Contig 15: 132417-134455 bp	Contig 16: 134556-135527 bp	Contig		
	17:				
	135628-189051 bp	Contig 18: 189152-189476 bp	Contig 19:		
	189577-191375 bp				
	Contig 20: 191476-201473 bp	Contig 21: 201574-202307 bp	Contig		
	22:				
	202408-204878 bp	Contig 23: 204979-213531 bp	Contig 24:		
	213632-218109 bp				
	Contig 25: 218210-219800 bp	Contig 26: 219901-220965 bp.			
	* NOTE: This is a 'working draft' sequence. It currently				
	* consists of 26 contigs. Gaps between the contigs				
	* are represented as runs of N. The order of the pieces				
	* is believed to be correct as given, however the sizes				
	* of the gaps between them are based on estimates that have				
	* provided by the submittor.				
	* This sequence will be replaced				
	* by the finished sequence as soon as it is available and				
	* the accession number will be preserved.				
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	* 11832	26218: contig of 14387 bp in length			
	* 26219	26318: gap of 100 bp			
	* 26319	28347: contig of 2029 bp in length			
	* 28348	28447: gap of 100 bp			
	* 28448	42160: contig of 13713 bp in length			
	* 42161	42360: gap of 200 bp			
	* 42361	55059: contig of 12699 bp in length			
	* 55060	55159: gap of 100 bp			
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* 61579 61678: gap of 100 bp
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* 117756 118727: contig of 972 bp in length
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* 189477 189576: gap of 100 bp
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* 191476 201473: contig of 9998 bp in length
* 201474 201573: gap of 100 bp
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VERSION AF224497.1 GI:13924486
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Hominidae; Homo.
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AUTHORS Scotet,E.J.
TITLE CCR3 expression is associated with chromatin remodeling in Th2
cells
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 7010)
AUTHORS Scotet,E.J.
TITLE Direct Submission
JOURNAL Submitted (13-JAN-2000) Basel Institute for Immunology, 487
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QY	2933	AATCTAG	TGACAG	AGAAATG	GCATG	ATAGAC	CTAAAG	CTAGCC
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QY	2993	TTTACT	TGTTAG	AGATTT	TGAACAA	ATTACT	TAAATTT	CTTCCCAT
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LOCUS AX345239 7201 bp DNA linear PAT 01-FEB-2002
DEFINITION Sequence 310 from Patent WO0200928.
ACCESSION AX345239
VERSION AX345239.1 GI:18493125
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE
1
AUTHORS Olek,A., Piepenbrock,C. and Berlin,K.
TITLE Diagnosis of diseases associated with the immune system
JOURNAL Patent: WO 0200928-A 310 03-JAN-2002;
Epigenomics AG (DE)
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/note="chemically treated genomic DNA (Homo sapiens)"
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Best Local Similarity 80.6%; Pred. No. 0;
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RESULT 12
AX345238
LOCUS AX345238 7201 bp DNA linear PAT 01-FEB-2002
DEFINITION Sequence 309 from Patent WO0200928.
ACCESSION AX345238
VERSION AX345238.1 GI:18493124
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS Olek,A., Piepenbrock,C. and Berlin,K.
TITLE Diagnosis of diseases associated with the immune system
JOURNAL Patent: WO 0200928-A 309 03-JAN-2002;
EpiGenomics AG (DB)
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/note="chemically created genomic DNA (Homo sapiens)"
ORIGIN
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Query Match 63.4%; Score 2271.8; DB 6; Length 7201;
Best Local Similarity 78.2%; Pred. No. 0;
Matches 2805; Conservative 0; Mismatches 772; Indels 10; Gaps 6;
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 DB 1454 GGAATTTTATTTTATTTATAGAGTTAGGGGGTATGAGCGTTTGTGTAAGATGGGA 1513
 QY 61 CCCCCAAGGAATGTCTCCCTGTGGGCACTTCCCTTACCAAGATGGGATGGCCAGTGGCTT 120
 DB 1514 TTTTAAAGGAATGTTTTTGT -GGTAATTTTATTTAGATGGGATGGTATGTAATT 1572
 QY 121 AAGTTGGTGTGTCAGGAGAAAAGATCTAGTTGTACTCTTGAGAGTTCCCGTTT 180
 DB 1573 AAGTTGGTGTAGGTAGAAAAAAGATTTAGTTGTATTTTGAGAGTTTTCGGTTT 1632
 QY 181 GTTCATGGCATGGGACAGGAGTCAAGAGCAGCAGCCTTGCTCACTGCTTACCAGTGA 240
 DB 1633 GTTTATGGTATGGGTAGGGAGTTAAGAGTAGTAGTTTGTTTAGTGTATTATTTAGTGA 1692
 QY 241 GGAAGAGGTGCATAGCCTGGGCGCAGGGCCAGGGCCCTGTGTGAGGCGTAGTGTAAACA 300
 DB 1693 GGAAGAGGTGTATAGTTTGGGTC - - GTTAGGGTTTGTGTGAGGCGTAGTGTAAATGA 1749
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 QY 361 TACAAACCAACACAGCAGGTTCCAGAAAAAGGCTCAGCGTTGGAACCAAGTCACCCCAC 420
 DB 1810 TATTAATTTATTTATAGTAGGTTTGAAGAAAAAGGTTTACCGTTGGAATTAAGTTATTTTAT 1869
 QY 421 TCAGCAGACACCAAGTATATTAATCAAGACCAACAGAGACAGAAACACCCCTTCCCA 480
 DB 1870 TTAGTAGATATTTAGTATATTAATTAAGAGATTAAATAGAGATAGAAATATTTTATTTTGA 1929
 QY 481 CTCTGCCCATGTCTCAAGTTGTAGTGGCCCTTCTCCAGATCTCTGCCACCATCTTGA 540
 DB 1930 TTTTGTTTTATGTTTTAAGTGTAGTGGTTTTTTTTTTAGATTTTGTATTATTTTGA 1989
 QY 541 AAGGACACTGAAAAGAGAACTGAAATTATTAAGCTGACAGACTAAAGAGAGATGATAAA 600
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 DB 2405 GGTATTTTGAAGGTTTAATTTAAATTTTATTTATTTGTATTTAAGTATTTATTTTG 2464
 QY 1021 ATTGAGCTGGGTAGACAGGTGAAAACTATATCAGGTTTTTAAATTTTAAATTTTAAAT 1080
 DB 2465 ATTGAGATGGGTAGATAGGTGAAAAATTAATATTAAGGTTTTTAAATTTTAAATTTTAAAT 2524

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 DB 2525 ATTTATTTATTTATTTATTTTGTAGATGAGTGTGGTGTCTGTTAGGTTGAGTGTAG 2584
 QY 1141 CGGCGTATCACAGTTTCACTGCAAGCCCTCAACCTTTCTAGGCTCAAGGGATTTCCCACTC 1200
 DB 2585 CGGCGTATTAAGTTATTTAGTTAGTTTAAATTTTAAAGGATTTTATTTT 2644
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 DB 2765 TGAATTTTATTTATTTGGTTTTTAAAGTATGGGATTAAGGTAAAGTTTTTT 2824
 QY 1381 GCCCATATGAGATTTTCTGTCTGTATCCCATGCACTAGTAAATCAAGACTTGGCTCT 1440
 DB 2825 GTTTATATGAGATTTTGTGTTTTTGAATTTATGTAGTTAGTAAATTAAGGATTTGGTTGT 2884
 QY 1441 GACTCTGAGAGACCTGCATGCTTCTTGAGCTGTGAATTCAGTCTAAGAGCTCATAGG 1500
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 QY 1801 AATGTATTTTTTTTTCTCAGCTGATGATTTGATTAATGCTATTAATGAATAAATGC 1860
 DB 3245 AATGTATTTTTTTTTTATGTTGATGATTTGATTAATGCTATTAATGAATAAATGC 3304
 QY 1861 TGAATGAGACACACAAACCAATTTGTCCCTCAGTCCATTTTCTCTCAAAAGCTGGA 1920
 DB 3305 TGAATGAGATATATATAATTAATTTGTTTTTATGTTTTTTTTTAAAGTTTGA 3364
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 DB 3365 ATGTGTTATGATTAAGTGGAGATGTATTTGATAGATTTATGAAGAAAGATTAATAGT 3424
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 QY 2041 TTCAATCTGCTTCTTACCAAGTTTAAACAGCTTTTCTGTGTTCAAAATGTGAATCAATA 2100
 DB 3485 TTTATTTTGTTTTATATAGTTTAAAGTTTGTGTTTAAATGTGAATTAATATA 3544
 QY 2101 CACTCTATTTTCTCTCATCAACCAAGTGAACCAATGCTCTCACTTGCATATAA 2160
 DB 3545 TATTTTATTTTATTTTATTAATAATTTTAAGTGAATTAATGCTTTTATTTTCGATATAA 3604
 QY 2161 GTAAAGAGGCTCTGCATTAAGGCTGTCTCAAGGCAAGCAAGCTGAGAGGCGTAGACT 2220

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Db      3725 TTTTAGATTCGATTAATTAATTTTAAAGAAGTAAATTAATTTTTCGATTTGGTTTA 3784
Qy      2341 GTTATTAAGCATTTCTCAGATTTAAGAAATGCCACGCGCTGTATATTACATC 2400
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Db      3845 TTTATTTTGTGTTTTTTTTTTTGAAGAGAGAAAGTATGATGATTTTGAAGAAAT 3904
Qy      2461 AGTCATGCGCTTAATCTGTCCCTCCATGACTCCTGCTTATCTGTTTCTATTTCCCT 2520
Db      3905 AGTGTATGGTTTAATTGTTTTTTTATGATTTTGTGTTTATTTGTTTTTTT 3964
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Qy      3061 ATGAATGCTCATCATTTATGCGGCTTGAGAGAGCATTAATTAATTTGTAATTAATC 3120
Db      4505 ATGAATGCTTATTTATTTATGCGGCTTGAGAGAGTAAATTAATTTGTAATTAAT 4564
Qy      3121 ATTGTTATTTATTTATTTATCATATTTTGTCTTTTAAATGATAAGATTTTAAAGTAT 3180
Db      4565 ATTGTTATTTATTTATTTATTTGTTTAAATGATAAGATTTTAAAGTATATG 4624
Qy      3181 TAAACTGTAAACATAAATGCAAAATGCCGTAAAGAGACAGTAGTAATAATGATTAT 3240
Db      4625 TAAATTTGTAATAATTAATGTAATAATGCTAAGAGATAGTAATAATAATGATTAT 4684
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Db      4805 ATGCGGGTATGTTAATTTGAAGTTTATGTTTTTTTTTTTTTAAATTTTGTG 4864
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Db      4925 GTATTTTGTGAGTATGATGAATAATTAATTTGTTGTTGTTTACGAAGATGATTATG 4984
Qy      3540 TCATTTGGGATTTGATTTTCTTCTTATCACAGGAGAGAGTGA 3586
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RESULT 13
AF262300
LOCUS      1310 bp mRNA linear PRI 26-JUN-2002
DEFINITION Homo sapiens clone 2 CC chemokine receptor 3 (CCR3) mRNA, partial cds.
ACCESSION AF262300
VERSION AF262300.1 GI:19171642
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominae; Homo.
REFERENCE   1 (bases 1 to 1310)
AUTHORS    Vijn,S., Dayhoff,D.E., Wang,C.E., Imam,Z., Ehrenberg,P.K. and
            Michael,N.L.
            Transcription Regulation of Human Chemokine Receptor CCR3: Evidence
            for a Rare TATA-less Promoter Structure Conserved between
            Drosophila and Humans
            Genomics 80 (1), 86-95 (2002)
JOURNAL     12079287
PUBMED     12079287
REFERENCES 2 (bases 1 to 1310)
AUTHORS    Vijn,S., Dayhoff,D.E., Wang,C.E., Ehrenberg,P.K. and Michael,N.L.
            Direct Submission
            Submitted (23-MAR-2000) Dept. of Mol. Diag. and Pathogenesis,
            Walter Reed Army Institute of Research, 1600 B. Gude Drive,
            Rockville, MD 20850, USA
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DB	23 TTAGCAGCTGCTATGATTTGATTAATGCTATTATGAATAAGAAATGCTGATGGAGCACAC					82
QY	1875 ACAAAACCATTTGTTCTTCAGTCCATTTTCTCCTCAAAAGCCTGGAATGTGCCATTGATC					1934
DB	83 ACAAAACCATTTGTTCTTCAGTCCATTTTCTCCTCAAAAGCCTGGAATGTGCCATTGATC					142
QY	1935 AGTGGAGATGTACCTGAGACAGACCCATGAAAAGAGATCAAGTCCACCCCAAGGAC					1994
DB	143 AGTGGAGATGTACCTGAGACAGACCCATGAAAAGAGATCAAGTCCACCCCAAGGAC					202
QY	1995 CCTATTTTCTTAATTTCAATTTGAATGGCTTCTAATTTGCTCTTTTCATTCTGCTTC					2054
DB	203 CCTATTTTCTTAATTTCAATTTGAATGGCTTCTAATTTGCTCTTTTCATTCTGCTTC					262
QY	2055 CTACCAAGTTTACAGCTTTTCTGGTTTCAAAATGTGAATCTACATCACTCTCATTTTTC					2114
DB	263 CTACCAAGTTTACAGCTTTTCTGGTTTCAAAATGTGAATCTACATCACTCTCATTTTTC					322
QY	2115 CTGATCACAACCCCAAGTGACCCAAATGGTCTCACTTTCGATATTAAGTAAGAGGCTCT					2174
DB	323 CTGATCACAACCCCAAGTGACCCAAATGGTCTCACTTTCGATATTAAGTAAGAGGCTCT					382
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DB	383 GCATTAAGGGCTTGTCCAAAGGACGAGCTGAGAGGCGCTAGACTGGCTCCATTTCAT					442
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DB	503 CAATTAATCTATTAAGAAAGCAAAACAATTCGCCGCATTGGCCCCAGTTATTAAGCATTT					562
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DB	623 TTCTCTCTAGAAAAGGAGAAAGTCAGTTGGATGCCCTCTGAGAACTAGTGCATGGCTTAA					682
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DB	683 CTGTCTCTCATGACTCCTGCCCTAATCTGTTTTCTATTTTCTTCCTTTTCCACCGAAGTC					742
QY	2535 TATTAATCTCAAGAAAAGCAGGCACTGGCCTTAGGGCTCCTGGCTAAGAAATATCAAGTC					2594
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QY	2595 CAGTGAGAAATCCCATTTGACTGACCCCTCTGCTTACCCCTTTGTGATGAGAAAGCTCCC					2654
DB	803 CAGTGAGAAATCCCATTTGACTGACCCCTCTGCTTACCCCTTTGTGATGAGAAAGCTCCC					862
QY	2655 AGGGGTTGCTTTTGTGATGTTACAGGCTTAATCTCAGCATCACAGGGGCAAGAAAAGG					2714
DB	863 AGGGGTTGCTTTTGTGATGTTACAGGCTTAATCTCAGCATCACAGGGGCAAGAAAAGG					922
QY	2715 AAAGTAACCTAAACTAATGCTGCTTAATTTGTAATTTGTAATTAATTACTGTGA					2774
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QY	2775 TTGTACATGTGTAAACAGCAAAATGTGTAATTTTTCACAGCTGCTGTGATTGGATTAT					2834
DB	983 TTGTACATGTGTAAACAGCAAAATGTGTAATTTTTCACAGCTGCTGTGATTGGATTAT					1042

QY	2835 GCCATTGGAAATAGATGCTGTTAAGACACACAGCCAGGTTCTCAAG	2885
DB	1043 GCCATTGGAAATAGATGCTGTTAAGACACACAGCCAGGTTCTCAAG	1093

RESULT 14
AF262304
LOCUS
DEFINITION
Homo sapiens clone 7 CC chemokine receptor 3-like mRNA, partial
sequence, alternatively spliced.
AF262304
AF262304.1 GI:19171650
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
AUTHORS
1 (bases 1 to 436)
Vijh,S., Dayhoff,D.E., Wang,C.E., Iman,Z., Ehrenberg,P.K. and
Michael,N.L.
TITLE
Transcription Regulation of Human Chemokine Receptor CCR3: Evidence
for a Rare TATA-less Promoter Structure Conserved between
Drosophila and Humans
Genomics 80 (1), 86-95 (2002)
12079287
JOURNAL
PUBMED
2 (bases 1 to 436)
Vijh,S., Dayhoff,D.E., Wang,C.E., Ehrenberg,P.K. and Michael,N.L.
AUTHORS
DIRECT SUBMISSION
TITLE
Submitted (23-MAR-2000) Dept. of Mol. Diag. and Pathogenesis,
Walter Reed Army Institute of Research, 1600 B. Gude Drive,
Rockville, MD 20850, USA
FEATURES
source
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ORIGIN

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QY	2809 TTCAAGCTGCTGTGATTTGATTAATGCCATTTGGAATAGAATGCTGTTAAGACACAC					2868
DB	72 TTTTCAGCTGCTGTGATTTGATTAATGCCATTTGGAATAGAATGCTGTTAAGACACAC					131
QY	2869 AAGCCAGTTCCTCAAGTCCGTAGCAAAATTTTCAAAAAGTTAAATTTAAAAATCACTACA					2928
DB	132 AAGCCAGTTCCTCAAGGCCGTAGCAAAATTTTCAAAAAGTTAAATTTAAAAATCACTACA					191
QY	2929 TTTGAATCTAGTACAGAGAAATGACATGATAGAGACTAAAGATCTAGCCCAAATTT					2988
DB	192 TTTGAATCTAGTACAGAGAAATGACATGATAGAGACTAAAGATCTAGCCCAAATTT					251
QY	2989 TATATTTACTTGTAGAGATTTTGAACAAATTAATTTCTTCAAGGTTCAATTTCC					3048
DB	252 TATATTTACTTGTAGAGATTTTGAACAAATTAATTTCTTCAAGGTTCAATTTCC					311
QY	3049 CCATTAATAATGAATGCTCATCATTTATGGGGCCCTGGAGAAACATAATTACTTTGA					3108
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RESULT 15

AR584940 1915 bp mRNA linear PAT 15-DEC-2004
LOCUS AR584940
DEFINITION Sequence 3 from patent US 6797811.
ACCESSION AR584940
VERSION AR584940.1 GI:56627916
KEYWORDS

SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1915)
AUTHORS Gray, P.W., Schweickart, V.L. and Raport, C.J.
TITLE Antibodies to chemokine receptor 88C
JOURNAL Patent: US 6797811-A 3 28-SEP-2004;
Icos Corporation; Bothell, WA

FEATURES
Source location/Qualifiers
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/organism="unknown"
/mol_type="mRNA"

ORIGIN
Query Match 9.6%; Score 344.2; DB 6; Length 1915;
Best Local Similarity 98.9%; Pred. No. 2.1e-59;
Matches 357; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

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Db 1 AATAATGATTATTATATTGTTATCATCTAGCCCTGTTTTCCTGTGTGATTTTC 60
QY 3287 TTCCCTTAAATGCTTACAGAAATCTGTATCCCATTCCTTACCAACCACCAACATTT 3346
Db 61 TTCCCTTAAATGCTTACAGAAATCTGTATCCCATTCCTTACCAACCACCAACATTT 120
QY 3347 CTGCTCTTTTCCCATGCC-GGTCAAGCTAACCTTGAAGCTTCAGCTCTTCCTCCTC 3405
Db 121 CTGCTCTTTTCCCATGCCGGGTGTAAGTAACTTGAAGCTTCAGCTCTTCCTCCTC 180
QY 3406 AATCCTTCTCCTGGCACCTCTGATATGCTTTTGAATTCATGTTAAGAATCCCTAGGC 3465
Db 181 AATCCTTCTCCTGGCACCTCTGATATGCTTTTGAATTCATGTTAAGAATCCCTAGGC 240
QY 3466 TGCTATCATGTGGCATCTTGTGAGTACATGAATAAATCACTGGTGTGTTTACGA 3525
Db 241 TGCTATCATGTGGCATCTTGTGAGTACATGAATAAATCACTGGTGTGTTTACGA 300
QY 3526 AGGATGATTATGCTTCATTTGGGAGTGTATTTTCTTCTTATCA CAGGAGAGTGA 3585
Db 301 AGGATGATTATGCTTCATTTGGGAGTGTATTTTCTTCTTATCA CAGGAGAGTGA 360
QY 3586 A 3586
Db 361 A 361

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